

Qy 2 SSNLS 7
Db 5 SSNLS 10

RESULT 38
ID ABM55576 standard; protein; 83 AA.
XX ABM55576;

XX 20-OCT-2003 (first entry)

XX Propionibacterium acnes predicted ORF-encoded polypeptide #20252.

XX Acne vulgaris; antisborrheic; dermatological; antibacterial;

XX Immunostimulant; Immune response; vaccine.

XX Propionibacterium acnes.

XX WO2003033515-A1.

XX 24-APR-2003.

XX 11-OCT-2002; 2002WO-US032727.

XX 15-OCT-2001; 2001US-00978825.

XX (CORI-) CORIXA CORP.

XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL,

XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D,

XX Barch B, Vallette-Douglase J;

XX WPI; 2003-381789/36.

XX N-PSDB; ACP64526.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.

XX Example 1; SEQ ID NO 20252; 1481bp; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACP64733)
XX encoding a Propionibacterium acnes protein. The invention also relates to
XX polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX immunogenic fragments of P. acnes polypeptides. The invention

XX additionally encompasses expression vectors and host cells comprising a
XX polynucleotide of the invention; antibodies against polypeptides of the
XX invention; fusion proteins comprising a polypeptide of the invention; a
XX method for stimulating an immune response specific for a P. acnes

XX polypeptide and an isolated T cell population comprising T cells prepared
XX via this method; a vaccine composition (comprising P. acnes polypeptides,
XX polynucleotides, antibodies, fusion proteins, T cell populations, or

XX antigen-presenting cells that express the polypeptide); a method and kit
XX for detecting or determining the presence or absence of P. acnes in a
XX patient; and a method for inhibiting the development of P. acnes in a

XX patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX proteins, T cell populations or antigen-presenting cells that express the
XX polypeptides are useful for diagnosing, preventing or treating acne

XX vulgaris, or for stimulating an immune response specific for a P. acnes
XX protein. The polynucleotides can also be used as probes or primers for
XX nucleic acid hybridization. The vaccine composition is useful for the

XX stimulation of an immune response against P. acnes, or for treating acne,
XX and the kit is useful for performing a diagnostic assay. The present
XX sequence represents a polypeptide predicted to be encoded by an ORF (open

XX reading frame) contained within the P. acnes polynucleotides of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pat_sequences

XX Sequence 83 AA;

Query Match 81.1%; Score 30; DB 6; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSNLS 7
Db 5 SSNLS 10

RESULT 39
ID ABU27913 standard; protein; 167 AA.
XX ABU27913;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #13440.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Enterobacter cloacae.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA31783.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 55837; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:

XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway

XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies

XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent

XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 167 AA;

Query Match 81.1%; Score 30; DB 6; Length 167;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLT 6
|:|:|
19 YASNLT 24
Db

RESULT 40
AAG49871
ID AAG49871 standard; protein; 182 AA.
XX
AC AAG49871;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63135.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
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PR 28-OCT-1999; 99US-0161993P.
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Query Match 81.1%; Score 30; DB 3; Length 182;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
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 Db 100 FSTNLS 106

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GenCore version 5.1.6
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Title: US-10-089-500-7

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SUMMARIES

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5	34	91.9	273	2	US-08-403-853-18
6	33	89.2	474	4	US-09-823-823-24
7	32	86.5	36	4	US-09-570-921-100
8	32	86.5	489	1	US-08-434-702-4
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14	30	81.1	238	4	US-09-270-767-45029
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17	30	81.1	609	4	US-09-198-452A-579
18	30	81.1	741	4	US-09-328-352-5898
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22	29	78.4	107	2	US-08-652-558-35
23	29	78.4	107	3	US-09-254-189-1
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26	29	78.4	496	4	US-09-710-279-1386
27	29	78.4	497	3	US-09-134-001C-4411

28	29	78.4	677	2	US-08-522-269B-3	Sequence 3, Appl1
29	29	78.4	677	3	US-09-294-923-3	Sequence 3, Appl1
30	29	78.4	747	3	US-09-291-922-2	Sequence 2, Appl1
31	28	75.7	7	1	US-08-137-117D-118	Sequence 118, Appl
32	28	75.7	7	2	US-08-480-434-78	Sequence 78, Appl
33	28	75.7	7	2	US-08-436-717-118	Sequence 118, Appl
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36	28	75.7	7	3	US-08-649-100-29	Sequence 29, Appl
37	28	75.7	7	4	US-09-563-222C-39	Sequence 39, Appl
38	28	75.7	32	3	US-08-525-539A-14	Sequence 14, Appl
39	28	75.7	98	4	US-09-134-000C-5271	Sequence 5271, Ap
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44	28	75.7	107	1	US-08-458-516-8	Sequence 8, Appl1
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ALIGNMENTS

RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAKORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-103
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-10
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
Db 70 YSSNLHS 76
RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO

APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMAWA, YOSHIOHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/225,322B
CURRENT FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:light chain
US-09-225-322B-19

Query Match 100.0%; Score 37; DB 4; Length 128;
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Db 70 YSSNLS 76

RESULT 3
US-09-764-304-10
Sequence 10, Application US/09764304
Patent No. 6495666
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMAWA, YOSHIOHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA KM-641
US-09-764-304-10

Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred.No.5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 4
US-09-764-304-19
Sequence 19, Application US/09764304
Patent No. 6495666
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMAWA, YOSHIOHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain
OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred.No.5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 5
US-08-403-853-18
Sequence 18, Application US/08403853
Patent No. 5844094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: KORRT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Rodyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-853-18

Query Match 91.9%; Score 34; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
Db 208 YTSNNLHS 214

RESULT 6
US-09-823-823-24
Sequence 24, Application US/09823823
Patent No. 6635904
GENERAL INFORMATION:
APPLICANT: Yamamoto, Satoshi
APPLICANT: Kasai, Hiroaki
APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Hamada, Tohtu
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING G
FILE REFERENCE: 12817-004001
CURRENT APPLICATION NUMBER: US/09/823,823
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/208,688
PRIOR FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: JP 97/343316
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 2.0
SEQ ID NO 24
LENGTH: 474
TYPE: PRT
ORGANISM: Cytophaga lycica
US-09-823-823-24

Query Match 89.2%; Score 33; DB 4; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSNNLHS 7
Db 164 YSNNLHS 170

RESULT 7
US-09-570-921-100
Sequence 100, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100
LENGTH: 36
TYPE: PRT
ORGANISM: Human
US-09-570-921-100

Query Match 86.5%; Score 32; DB 4; Length 36;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
Db 16 YTSNNLHS 22

RESULT 8
US-08-434-702-4
Sequence 4, Application US/08434702
Patent No. 5554743
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Fischer, Robert L.
APPLICANT: Lashbrook, Coralie
TITLE OF INVENTION: Endo-1,4-beta-Glucanase Genes and Their
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,702
FILING DATE: 04-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,883
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,466
FILING DATE: 18-APR-1991

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,417
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 02307E-30430US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-5043
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-434-702-4

Query Match      86.5%; Score 32; DB 1; Length 489;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLS 7
Db      216 YSSLS 222

RESULT 9
US-09-495-406-13
; Sequence 13, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-09-495-406-13

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLS 7
Db      268 FSSNLS 274

RESULT 10
US-09-816-028A-17
; Sequence 17, Application US/09816028A
; Patent No. 6699705
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-09-816-028A-17
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; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-17

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLS 7
Db      268 FSSNLS 274

RESULT 11
US-10-303-162-17
; Sequence 17, Application US/10303162
; Patent No. 6723545
; GENERAL INFORMATION:
; APPLICANT: Wakarchuk, Michel
; APPLICANT: Gilbert, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/10/303,162
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-162-17

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLS 7
Db      268 FSSNLS 274

RESULT 12
US-09-248-796A-22868
; Sequence 22868, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
```

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; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22868
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-22868

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
Db 44 YSNLH 49

RESULT 13
US-09-270-767-41649
; Sequence 41649, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41649
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-41649

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 172;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
Db 157 YSNLH 162

RESULT 14
US-09-270-767-45029
; Sequence 45029, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45029
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-45029

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 238;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YSSNLS 7
Db 232 YSNLH 238

RESULT 15
US-09-252-991A-28155
; Sequence 28155, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28155
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-28155

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 410;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
Db 260 YSNLH 265

RESULT 16
US-09-538-092-1356
; Sequence 1356, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafastSeqformatler Version 0.9
; SEQ ID NO 1356
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16600
; US-09-538-092-1356

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 458;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLS 7
Db 443 SSNLS 448

RESULT 17
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US-09-198-452A-579
; Sequence 579, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Giffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 579
; LENGTH: 609
; TYPE: PRF
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...609
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-579

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 609;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLS 7
Db 126 SSNLS 131

RESULT 18
US-09-328-352-5898
; Sequence 5898, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5898
; LENGTH: 741
; TYPE: PRF
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5898

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 741;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6
Db 512 YSSNLH 517

RESULT 19
US-08-630-915A-30
; Sequence 30, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-30

Query Match
Best Local Similarity 81.1%; Score 30; DB 3; Length 788;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 7
Db 388 YSSNLH 394

RESULT 20
US-09-879-957-30
; Sequence 30, Application US/09879957
; Patent No. 6709821
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6709821h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915

FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Miarock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-879-957-30

Query Match 81.1%; Score 30; DB 4; Length 788;
Best Local Similarity 71.4%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLHS 7
Db 388 YSSNPHA 394

RESULT 21
US-08-652-558-2
Sequence 2, Application US/08652558
Patent No. 586155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-2

Query Match 78.4%; Score 29; DB 2; Length 107;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 YSSNLHS 7
Db 50 YTSLSHS 56

RESULT 22
US-08-652-558-35
Sequence 35, Application US/08652558
Patent No. 586155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-35

Query Match 78.4%; Score 29; DB 2; Length 107;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLHS 7
Db 50 YTSLSHS 56

RESULT 23
US-09-254-189-1
Sequence 1, Application US/09254189
Patent No. 6150792
GENERAL INFORMATION:
APPLICANT: Lundquist, Tomas
TITLE OF INVENTION: Sequence Listing
FILE REFERENCE: 3526/00000
CURRENT APPLICATION NUMBER: US/09/254,189
EARLIER FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 00/000,000
NUMBER OF SEQ ID NOS: 6

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; US-09-254-189-1

Query Match
Best Local Similarity 78.4%; Score 29; DB 3; Length 107;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 50 YTSLSLS 56

RESULT 24
US-09-270-767-45934
; Sequence 45934, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45934
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-45934

Query Match
Best Local Similarity 78.4%; Score 29; DB 4; Length 219;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 146 YATNHS 152

RESULT 25
US-09-252-991A-21191
; Sequence 21191, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21191
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-21191

Query Match
Best Local Similarity 78.4%; Score 29; DB 4; Length 329;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 YSSNLS 7
DB 188 YSRNLHT 194

RESULT 26
US-09-710-279-1386
; Sequence 1386, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1386
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-710-279-1386

Query Match
Best Local Similarity 78.4%; Score 29; DB 4; Length 496;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 274 YDSNLS 279

RESULT 27
US-09-134-001C-4411
; Sequence 4411, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4411
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-4411

Query Match
Best Local Similarity 78.4%; Score 29; DB 3; Length 497;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 275 YDSNLS 280

RESULT 28
US-08-522-269B-3
; Sequence 3, Application US/08522269B
; Patent No. 5919690
```


GENERAL INFORMATION:
APPLICANT: Knapp, Inge Helmer
APPLICANT: Hjort, Carsten M.
APPLICANT: Halkier, Torben
APPLICANT: Kofoed, Lene Venke
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: No. 59196900 No. 59196900dsk of No. 59196900th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,269B
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valecia A.
REGISTRATION NUMBER: 37,125
REFERENCE/DOCKET NUMBER: 3935.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-522-269B-3

Query Match 78.4%; Score 29; DB 2; Length 677;
Best Local Similarity 71.4%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0

OY 1 YSSNLS 7
DB 212 YSSHLN 218

RESULT 29
US-09-294-923-3
Sequence 3, Application US/09294923
Patent No. 6197566
GENERAL INFORMATION:
APPLICANT: Knapp, Inge Helmer
APPLICANT: Hjort, Carsten M.
APPLICANT: Halkier, Torben
APPLICANT: Kofoed, Lene Venke
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: No. 61975660 No. 6197566dsk of No. 6197566th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,923

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/522,269
FILING DATE: 12-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valecia A.
REGISTRATION NUMBER: 37,125
REFERENCE/DOCKET NUMBER: 3935.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-294-923-3

Query Match 78.4%; Score 29; DB 3; Length 677;
Best Local Similarity 71.4%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0

OY 1 YSSNLS 7
DB 212 YSSHLN 218

RESULT 30
US-09-291-922-2
Sequence 2, Application US/09291922
Patent No. 6183776
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Hiltz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
CURRENT APPLICATION NUMBER: US/09/291,922
EARLIER FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 60/083,044
EARLIER FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 747
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: UNSURE
LOCATION: (129)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (133) .. (134)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (144)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (178)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (207)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (218)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (220)
FEATURE:

NAME/KEY: UNSURE
LOCATION: (236)
US-09-291-922-2

Query Match 78.4%; Score 29; DB 3; Length 747;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
DB 368 YEDNLS 374

RESULT 31
US-08-137-117D-118
Sequence 118, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masaayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SAIDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-137-117D-118

Query Match 75.7%; Score 28; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSNNLHS 7
DB 1 YSNNLHS 7

DB 1 YTSRLHS 7

RESULT 32
US-08-480-434-78
Sequence 78, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. DiIow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halliwin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-78

Query Match 75.7%; Score 28; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
DB 1 YTSRLHS 7

RESULT 33
US-08-436-717-118
Sequence 118, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masaayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SAIDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-118

Query Match 75.7%; Score 28; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 1 YTSRLHS 7

RESULT 34
US-08-053-451B-78
Sequence 78, Application US/08053451B
Patent No. 595584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: D'Clow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B

FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-78

Query Match 75.7%; Score 28; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 1 YASRLHS 7

RESULT 35
US-08-649-100-13
Sequence 13, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-649-100-13

Query Match 75.7%; Score 28; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLS 7
|:|
1 YTSRLHS 7

RESULT 36
US-08-649-100-29
; Sequence 29, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-649-100-29

Query Match 75.7%; Score 28; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLS 7
|:|
1 YTSRLHS 7

RESULT 37
US-09-563-222C-39
; Sequence 39, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MITCH B.

US-09-563-222C-39

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-39

Query Match 75.7%; Score 28; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLS 7
|:|
1 YASRLHS 7

RESULT 38
US-08-525-539A-14
; Sequence 14, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-14

Query Match 75.7%; Score 28; DB 3; Length 32;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLSH 7
 DB 1 YTSRLHS 7

RESULT 39
 US-09-134-000C-5271

; Sequence 5271, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5271
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 US-09-134-000C-5271

Query Match 75.7%; Score 28; DB 4; Length 98;
 Best Local Similarity 57.1%; Pred. No. 2.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLSH 7
 DB 54 YANNLHA 60

RESULT 40
 US-09-248-796A-19786

; Sequence 19786, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstein et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 19786
 ; LENGTH: 99
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-19786

Query Match 75.7%; Score 28; DB 4; Length 99;
 Best Local Similarity 63.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLSH 6
 DB 23 YSSSLH 28

Search completed: December 17, 2004, 18:32:09
 Job time : 4.24719 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:20:33 / Search time 13.5281 Seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSSNLS 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	128	9	US-09-764-304-10
2	37	100.0	128	9	US-09-764-304-10
3	37	100.0	128	14	US-10-265-713-10
4	37	100.0	128	14	US-10-265-713-10
5	37	100.0	128	14	US-10-166-626-10
6	37	100.0	128	14	US-10-166-626-10
7	34	91.9	107	17	US-10-741-657A-16
8	34	91.9	2207	16	US-10-437-963-189767
9	33	89.2	91	15	US-10-424-599-201107
10	33	89.2	303	15	US-10-424-599-208663
11	33	89.2	306	15	US-10-425-114-49623
12	33	89.2	474	9	US-09-823-829-24
13	33	89.2	474	9	US-09-823-823-24

ALIGNMENTS

14	33	89.2	503	16	US-10-437-963-197006	Sequence 197006,
15	32	86.5	47	17	US-10-425-115-227775	Sequence 227775,
16	32	86.5	59	15	US-10-424-599-190057	Sequence 190057,
17	32	86.5	500	10	US-09-970-367-2	Sequence 2, Appl1
18	31	83.8	61	17	US-10-425-115-316851	Sequence 316851,
19	31	83.8	277	15	US-10-282-122A-53384	Sequence 53384, A
20	31	83.8	347	9	US-09-816-028A-17	Sequence 17, Appl
21	31	83.8	347	14	US-10-303-161-17	Sequence 17, Appl
22	31	83.8	347	14	US-10-303-118-17	Sequence 17, Appl
23	31	83.8	347	14	US-10-303-128-17	Sequence 17, Appl
24	31	83.8	347	14	US-10-303-134-17	Sequence 17, Appl
25	31	83.8	347	14	US-10-303-152-17	Sequence 17, Appl
26	31	83.8	347	14	US-10-820-356-17	Sequence 17, Appl
27	31	83.8	347	17	US-10-845-408-17	Sequence 17, Appl
28	31	83.8	347	17	US-10-845-412-17	Sequence 17, Appl
29	31	83.8	347	17	US-10-846-219-17	Sequence 17, Appl
30	31	83.8	347	17	US-10-821-573-17	Sequence 17, Appl
31	31	83.8	347	17	US-10-821-604-17	Sequence 17, Appl
32	31	83.8	347	17	US-10-847-963-17	Sequence 17, Appl
33	31	83.8	385	17	US-10-425-115-320203	Sequence 320203,
34	31	83.8	385	17	US-10-739-930-7620	Sequence 7620, Ap
35	31	83.8	392	15	US-10-425-114-49028	Sequence 49028, A
36	31	83.8	407	15	US-10-425-114-64369	Sequence 64369, A
37	31	83.8	442	15	US-10-424-599-285570	Sequence 285570,
38	31	83.8	501	17	US-10-425-115-192258	Sequence 192258,
39	31	83.8	529	15	US-10-425-115-231545	Sequence 231545,
40	30	81.1	62	17	US-10-425-115-242547	Sequence 242547,
41	30	81.1	74	15	US-10-424-599-264246	Sequence 264246,
42	30	81.1	79	17	US-10-425-115-223534	Sequence 223534,
43	30	81.1	81	17	US-10-425-115-193189	Sequence 193189,
44	30	81.1	97	17	US-10-425-115-189365	Sequence 189365,
45	30	81.1	104	15	US-10-424-599-165308	Sequence 165308,

RESULT 1

US-09-764-304-10
Sequence 10, Application US/09764304
Patent No. US20020026036A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP-3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA KM-641
US-09-764-304-10

Query Match 100.0%; Score 37; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 2

US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 100.0%; Score 37; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 3
US-10-265-713-10

; Sequence 10, Application US/10265713
; Publication No. US2003009564A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31

; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

QY 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 4

US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US2003009564A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
; OTHER INFORMATION: variable region
US-10-265-713-19

Query Match 100.0%; Score 37; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMAWA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-166-626-10

Query Match 100.0%; Score 37; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
|:|||||
Db 70 YSSNLS 76

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMAWA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-166-626-19

Query Match 100.0%; Score 37; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
|:|||||
Db 70 YSSNLS 76

RESULT 7
US-10-741-657A-16
; Sequence 16, Application US/10741657A
; Publication No. US20040197325A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
; FILE REFERENCE: 05882.0177.NPUS01
; CURRENT APPLICATION NUMBER: US/10/741,657A
; CURRENT FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-741-657A-16

Query Match 91.9%; Score 34; DB 17; Length 107;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
|:|||||
Db 50 YTSNLS 56

RESULT 8
US-10-437-963-189767
; Sequence 189767, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nuclear Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189767
; LENGTH: 2207
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2207)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_23625C.1.pep
US-10-424-599-201107

Query Match 91.9%; Score 34; DB 16; Length 2207;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||
Db 850 YSNNLHS 856

RESULT 9

US-10-424-599-201107
Sequence 201107, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53223)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 201107

LENGTH: 91

TYPE: PRT

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: PAT_MRT3847_23625C.1.pep
US-10-424-599-201107

Query Match 89.2%; Score 33; DB 15; Length 91;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||
Db 8 FSSNNLHS 14

RESULT 10

US-10-424-599-200863

Sequence 200863, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53223)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 200863

LENGTH: 303

TYPE: PRT

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: PAT_MRT3847_30631C.1.pep
US-10-424-599-200863

Query Match 89.2%; Score 33; DB 15; Length 303;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||

Db 9 FSSNNLHS 15

RESULT 11

US-10-425-114-49629
Sequence 49629, Application US/10425114
Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53313)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 49629

LENGTH: 306

TYPE: PRT

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: 700739771_FLI.pep
US-10-425-114-49629

Query Match 89.2%; Score 33; DB 15; Length 306;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||
Db 12 FSSNNLHS 18

RESULT 12

US-09-823-829-24
Sequence 24, Application US/09823829
Patent No. US20020146697A1

GENERAL INFORMATION:

APPLICANT: Yamamoto, Satoshi

APPLICANT: Nakamura, Shoko

APPLICANT: Suzuki, Makoto

APPLICANT: Kasai, Hiroaki

APPLICANT: Hamada, Tohru

TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS

FILE REFERENCE: 12817-004001

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US 09/823,829

PRIOR FILING DATE: 1998-12-10

PRIOR APPLICATION NUMBER: JP 97/343316

NUMBER OF SEQ ID NOS: 82

SOFTWARE: PatentIn version 2.0

SEQ ID NO 24

LENGTH: 474

TYPE: PRT

ORGANISM: Cytophaga lytica

US-09-823-829-24

Query Match 89.2%; Score 33; DB 9; Length 474;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||
Db 164 YSNNLHS 170

RESULT 13
US-09-823-823-24
; Sequence 24, Application US/09823823
; Patent No. US20020171092A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Satoehi
; APPLICANT: Kasai, Hiroaki
; APPLICANT: Nakamura, Shoko
; APPLICANT: Suzuki, Makoto
; APPLICANT: Hamada, Tohtu
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING
; FILE REFERENCE: 12817-004001
; CURRENT APPLICATION NUMBER: US/09/823,823
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/208,688
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: JP 97/343316
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin version 2.0
; SEQ ID NO 24
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Cytophaga lycica
US-09-823-823-24

Query Match 89.2%; Score 33; DB 9; Length 474;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
; |||||
DB 164 YSENLS 170

RESULT 14
US-10-437-963-197006
; Sequence 197006, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbasuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197006
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92805C.1.pap
US-10-437-963-197006

Query Match 89.2%; Score 33; DB 16; Length 503;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
; |||||
DB 84 YSSNLS 89

RESULT 15

US-10-425-115-227775
; Sequence 227775, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 227775
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139326C.1.pap
US-10-425-115-227775

Query Match 86.5%; Score 32; DB 17; Length 47;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
; |||||
DB 12 HSSNLS 18

RESULT 16
US-10-424-599-190057
; Sequence 190057, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 265684
; SEQ ID NO 190057
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142640C.1.pap
US-10-424-599-190057

Query Match 86.5%; Score 32; DB 15; Length 59;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
; |||||
DB 9 YSSNLS 15

RESULT 17
US-09-970-367-2
; Sequence 2, Application US/09970367
; Publication No. US20030106092A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Eric L.
; APPLICANT: Goellner, Melissa
; TITLE OF INVENTION: ENDOGLUCANASE GENE PROMOTER UPREGULATED BY NEMATODES
; FILE REFERENCE: 5051.387
; CURRENT APPLICATION NUMBER: US/09/970,367

;; CURRENT FILING DATE: 2001-10-02
;; NUMBER OF SEQ ID NOS: 21
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 500
;; TYPE: PRT
;; ORGANISM: Nicotiana tabacum
US-09-970-367-2

Query Match 86.5%; Score 32; DB 10; Length 500;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 228 YSSSLHS 234

RESULT 18
US-10-425-115-316851
; Sequence 316851, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 316851
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_5203C.1.pcp
US-10-425-115-316851

Query Match 83.8%; Score 31; DB 17; Length 61;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 52 YSINLS 58

RESULT 19
US-10-282-122A-53384
; Sequence 53384, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/151,078
; PRIOR FILING DATE: 2000-03-21

;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53384
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53384

Query Match 83.8%; Score 31; DB 15; Length 277;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
Db 94 YSSNLS 99

RESULT 20
US-09-816-028A-17
; Sequence 17, Application US/09816028A
; Patent No. US20020042369A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-17

Query Match 83.8%; Score 31; DB 9; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 268 FSSNLS 274

RESULT 21
US-10-303-161-17
; Sequence 17, Application US/10303161
; Publication No. US20030148459A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,161
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-161-17

Query Match 83.8%; Score 31; DB 14; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLSHS 7
DB 268 PSSNHS 274

RESULT 22
US-10-303-118-17
; Sequence 17, Application US/10303118
; Publication No. US20030157655A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,118
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-118-17

Query Match 83.8%; Score 31; DB 14; Length 347;

Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLSHS 7
DB 268 PSSNHS 274

RESULT 23
US-10-303-128-17
; Sequence 17, Application US/10303128
; Publication No. US20030157656A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-128-17

Query Match 83.8%; Score 31; DB 14; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLSHS 7
DB 268 PSSNHS 274

RESULT 24
US-10-303-134-17
; Sequence 17, Application US/10303134
; Publication No. US20030157657A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,134
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni

```

; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-134-17

Query Match
Best Local Similarity 83.8%; Score 31; DB 14; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 268 FSSNHS 274

RESULT 25
US-10-303-162-17
; Sequence 17, Application US/10303162
; Publication No. US20030157658A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,162
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-162-17

Query Match
Best Local Similarity 83.8%; Score 31; DB 14; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 268 FSSNHS 274

RESULT 26
US-10-820-536-17
; Sequence 17, Application US/10820536
; Publication No. US20040203103A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/820,536
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: 10/303,128
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
```

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; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-820-536-17

Query Match
Best Local Similarity 83.8%; Score 31; DB 17; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 268 FSSNHS 274

RESULT 27
US-10-845-408-17
; Sequence 17, Application US/10845408
; Publication No. US20040203112A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/845,408
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-845-408-17

Query Match
Best Local Similarity 83.8%; Score 31; DB 17; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 268 FSSNHS 274

RESULT 28
US-10-845-412-17
; Sequence 17, Application US/10845412
; Publication No. US20040203113A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
```

;; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
;; FILE REFERENCE: 019633-000111US
;; CURRENT APPLICATION NUMBER: US/10/845,412
;; CURRENT FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: US/10/303,128
;; PRIOR FILING DATE: 2002-11-21
;; PRIOR APPLICATION NUMBER: US/09/816,028
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: US 60/118,213
;; PRIOR FILING DATE: 1999-02-01
;; PRIOR APPLICATION NUMBER: US 09/495,406
;; PRIOR FILING DATE: 2000-01-31
;; NUMBER OF SEQ ID NOS: 49
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 17
;; LENGTH: 347
;; TYPE: PRF
;; ORGANISM: Campylobacter jejuni
;; FEATURE:
;; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
;; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
;; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-845-412-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 268 FSSNLS 274

RESULT 29
US-10-846-219-17
;; Sequence 17, Application US/10846219
;; Publication No. US20040219638A1
;; GENERAL INFORMATION:
;; APPLICANT: Gilbert, Michel
;; APPLICANT: Makarchuk, Warren W.
;; APPLICANT: National Research Council of Canada
;; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
;; FILE REFERENCE: 019633-000111US
;; CURRENT APPLICATION NUMBER: US/10/846,219
;; CURRENT FILING DATE: 2004-05-14
;; PRIOR APPLICATION NUMBER: US/09/816,028
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: US 60/118,213
;; PRIOR FILING DATE: 1999-02-01
;; PRIOR APPLICATION NUMBER: US 09/495,406
;; PRIOR FILING DATE: 2000-01-31
;; NUMBER OF SEQ ID NOS: 49
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 17
;; LENGTH: 347
;; TYPE: PRF
;; ORGANISM: Campylobacter jejuni
;; FEATURE:
;; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
;; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
;; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-846-219-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 268 FSSNLS 274

RESULT 30
US-10-821-573-17
;; Sequence 17, Application US/10821573
;; Publication No. US20040229313A1
;; GENERAL INFORMATION:
;; APPLICANT: Gilbert, Michel
;; APPLICANT: Makarchuk, Warren W.
;; APPLICANT: National Research Council of Canada
;; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
;; FILE REFERENCE: 019633-000111US
;; CURRENT APPLICATION NUMBER: US/10/821,573
;; CURRENT FILING DATE: 2004-04-08
;; PRIOR APPLICATION NUMBER: US/09/816,028
;; PRIOR FILING DATE: 2002-11-21
;; PRIOR APPLICATION NUMBER: US/09/816,028
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: US 60/118,213
;; PRIOR FILING DATE: 1999-02-01
;; PRIOR APPLICATION NUMBER: US 09/495,406
;; PRIOR FILING DATE: 2000-01-31
;; NUMBER OF SEQ ID NOS: 49
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 17
;; LENGTH: 347
;; TYPE: PRF
;; ORGANISM: Campylobacter jejuni
;; FEATURE:
;; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
;; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
;; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-821-573-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 268 FSSNLS 274

RESULT 31
US-10-821-604-17
;; Sequence 17, Application US/10821604
;; Publication No. US20040229263A1
;; GENERAL INFORMATION:
;; APPLICANT: Gilbert, Michel
;; APPLICANT: Makarchuk, Warren W.
;; APPLICANT: National Research Council of Canada
;; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
;; FILE REFERENCE: 019633-000111US
;; CURRENT APPLICATION NUMBER: US/10/821,604
;; CURRENT FILING DATE: 2004-04-08
;; PRIOR APPLICATION NUMBER: US/09/816,028
;; PRIOR FILING DATE: 2002-11-21
;; PRIOR APPLICATION NUMBER: US/09/816,028
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: US 60/118,213
;; PRIOR FILING DATE: 1999-02-01
;; PRIOR APPLICATION NUMBER: US 09/495,406
;; PRIOR FILING DATE: 2000-01-31
;; NUMBER OF SEQ ID NOS: 49
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 17
;; LENGTH: 347
;; TYPE: PRF
;; ORGANISM: Campylobacter jejuni
;; FEATURE:
;; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
;; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
;; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-821-604-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-10-821-604-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 268 FSSNIHS 274

RESULT 32

US-10-847-983-17
; Sequence 17, Application US/10847983
; Publication No. US20040229272A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Makarchuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/847,983
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-847-983-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 268 FSSNIHS 274

RESULT 33

US-10-425-115-320203
; Sequence 320203, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 320203
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_55091C.1.pep
US-10-425-115-320203

Query Match 83.8%; Score 31; DB 17; Length 385;
Best Local Similarity 85.7%; Pred. No. 8.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 165 YSSNOHS 171

RESULT 34

US-10-739-930-7620
; Sequence 7620, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7620
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C21375_2.p
US-10-739-930-7620

Query Match 83.8%; Score 31; DB 17; Length 385;
Best Local Similarity 85.7%; Pred. No. 8.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 165 YSSNOHS 171

RESULT 35

US-10-425-114-49028
; Sequence 49028, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49028
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700726516_FLI.pep
US-10-425-114-49028

Query Match 83.8%; Score 31; DB 15; Length 392;
Best Local Similarity 85.7%; Pred. No. 8.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 195 YSSGLHS 201

RESULT 36
US-10-425-114-64369
; Sequence 64369, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64369
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-224-H11_F11.pep
US-10-425-114-64369

Query Match
Best Local Similarity 83.8%; Score 31; DB 15; Length 407;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 187 YSSNLS 193

RESULT 37
US-10-424-599-285570
; Sequence 285570, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 285570
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9989C.1.pep
US-10-424-599-285570

Query Match
Best Local Similarity 83.8%; Score 31; DB 15; Length 442;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 25 YSSNLS 31

RESULT 38
US-10-425-115-192258
; Sequence 192258, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 192258
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106925C.1.pep
US-10-425-115-192258

Query Match
Best Local Similarity 83.8%; Score 31; DB 17; Length 501;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 477 YSSNLS 483

RESULT 39
US-10-424-599-231545
; Sequence 231545, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231545
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51106C.1.pep
US-10-424-599-231545

Query Match
Best Local Similarity 83.8%; Score 31; DB 15; Length 529;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 332 YSSNLS 338

RESULT 40
US-10-425-115-242547
; Sequence 242547, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 242547

; LENGTH: 62
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_152789C.1.pep
US-10-425-115-242547

Query Match 81.1%; Score 30; DB 17; Length 62;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6
Db 40 YSTNLH 45

Search completed: December 17, 2004, 18:38:01
Job time : 14.5281 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 17, 2004, 18:11:22 ; Search time 2.75281 seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSSNLS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	89.2	219	2 T30122	hypothetical prote
2	33	89.2	368	2 G86895	hypothetical prote
3	32	86.5	324	2 S61447	cellulase (EC 3.2.
4	32	86.5	489	2 T06350	cellulase (EC 3.2.
5	31	83.8	107	2 A48677	Ig kappa chain V-J
6	31	83.8	380	2 A81198	conserved hypotet
7	31	83.8	380	2 A81833	conserved hypotet
8	30	81.1	243	2 AF0777	probable transcrip
9	30	81.1	290	2 A12054	hypothetical prote
10	30	81.1	313	2 T48439	probable RNA-bindi
11	30	81.1	412	2 S72617	alcohol dehydrogen
12	30	81.1	424	2 C86247	hypothetical prote
13	30	81.1	427	2 T23954	hypothetical prote
14	30	81.1	458	2 P97296	UDP-N-acetylmutam
15	30	81.1	459	2 AF2847	two component sens
16	30	81.1	459	2 E97624	osmolarity sensor
17	30	81.1	472	2 AD2532	hypothetical prote
18	30	81.1	816	2 T17257	hypothetical prote
19	30	81.1	844	2 B83136	probable fibrillar
20	30	81.1	1042	1 G86895	beta-galactosidase
21	30	81.1	1042	2 E85968	evolved beta-D-gal
22	30	81.1	1042	2 F91123	evolved beta-D-gal
23	30	81.1	1723	2 H86557	polymorphic membra
24	30	81.1	1723	2 E72067	polymorphic membra
25	30	81.1	1732	2 C81601	polymorphic membra
26	29	78.4	108	1 KVM573	Ig kappa chain V r
27	29	78.4	111	2 G38740	Ig kappa chain V r
28	29	78.4	111	2 A38740	Ig kappa chain V r
29	29	78.4	111	2 E38740	Ig kappa chain V r

30	29	78.4	111	2 C38740	Ig kappa chain V r
31	29	78.4	227	2 T11242	ribosomal protein
32	29	78.4	243	2 G89567	protein T08A9.2 [1
33	29	78.4	334	1 TVMSJA	transcription fact
34	29	78.4	334	2 S12742	transcription fact
35	29	78.4	347	2 T25192	hypothetical prote
36	29	78.4	391	2 T38822	hypothetical prote
37	29	78.4	451	2 B69675	glucose-6-phosphat
38	29	78.4	465	2 G96655	unknown protein, 2
39	29	78.4	516	2 T33061	hypothetical prote
40	29	78.4	550	2 P90407	molycoprotein bios
41	29	78.4	572	2 T51525	hypothetical prote
42	29	78.4	732	2 A12158	hypothetical prote
43	29	78.4	746	2 S74219	alpha-galactosidas
44	29	78.4	787	2 T00798	hypothetical prote
45	29	78.4	867	2 T14777	hypothetical prote

ALIGNMENTS

RESULT 1
T30122
hypothetical protein F22H10.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30122
R/Langston, Y.; Hawking, J.
submitted to the EMBL Data Library, September 1996
A/Description: The sequence of C. elegans cosmid F22H10.
A/Reference number: Z20740
A/Accession: T30122
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-219 <LAN>
A/Cross-references: UNIPROT:Q94192; EMBL:U70845; PIDD:AA09103.1; GSPDB:GN00028; CESP:F2;
A/Experimental source: strain Bristol N2; clone F22H10
C/Genetics:
A/Genes: CESP:F22H10.6
A/Map position: X
A/Introns: 47/1; 67/1; 107/3; 135/3

Query Match
Best Local Similarity 89.2%; Score 33; DB 2; Length 219;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 22 FSSNLS 28
:|||||

RESULT 2
G86895
hypothetical protein yweB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: G86895
R/Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A/Reference number: A86625; WUID:2135186; PMID:11337471
A/Accession: G86895
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-368 <STO>
A/Cross-references: UNIPROT:Q9CD01; GB:AE005176; PIDD:G12725228; PIDD:AA06265.1; GSPDB:G
A/Experimental source: strain IL1403
C/Genetics:
A/Genes: yweB

Query Match
Best Local Similarity 89.2%; Score 33; DB 2; Length 368;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 121 FSSNLS 127

RESULT 3
S61447
cellulase (EC 3.2.1.4) CX3 - pepper (fragment)
C:Accession: A48677
C:Species: Capsicum annuum (pepper)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S61447
R:Ferrarese, L.; Trinocci, L.; Moretto, P.; Polverino de Laureto, P.; Rascio, N.; Casad
Plant Mol. Biol. 29, 735-747, 1995
A:Title: Differential ethylene-inducible expression of cellulase in pepper plants.
A:Reference number: S61445; MUID:96128016; PMID:8541500
A:Accession: S61447
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-324 <PER>
A:Cross-references: UNIPROT:Q43751; EMBL:X83711
C:Superfamily: Arabidopsis membrane-anchored cellulase KOR
C:Keywords: glycosidase; hydrolase

Query Match 86.5%; Score 32; DB 2; Length 324;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 144 YSSNLS 150

RESULT 4
T06350
cellulase (EC 3.2.1.4) Cel2 precursor - tomato
N:Alternate names: endo-1,4-beta-glucanase
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
R:Hasbrook, C.C.; Gonzalez-Bosch, C.; Bennett, A.B.
Plant Cell 6, 1485-1493, 1994
A:Title: Two divergent endo-beta-1,4-glucanase genes exhibit overlapping expression in
A:Reference number: Z15614; MUID:95086382; PMID:7994180
A:Accession: T06350
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-489 <LAS>
A:Cross-references: UNIPROT:Q42872; EMBL:U13055; NID:9531904; PIDN:AAA69909.1; PID:95319
A:Experimental source: strain Castlemart; tissue-type pericarp
C:Genetics:
A:Gene: Cel2
C:Function:
A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A:Pathway: cellulose degradation
C:Superfamily: Arabidopsis membrane-anchored cellulase KOR
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-489/Product: cellulase 2 #status predicted <MAT>

Query Match 86.5%; Score 32; DB 2; Length 489;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 216 YSSNLS 222

RESULT 5
A48677
Ig kappa chain V-J region (48) - mouse (fragment)
C:Species: Mus musculus (mouse)

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C:Accession: A48677
R:Rasignon, J.; Braic, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A:Title: Molecular characterization of monoclonal CRI-A-positive anti-arsenate antibodies
A:Reference number: A48677; MUID:94022404; PMID:8415731
A:Accession: A48677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <TAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 31; DB 2; Length 107;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 50 YSSNLS 56

RESULT 6
A81198
conserved hypothetical protein NMB0455 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81198
R:Retlein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappelli, R.; Ver
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: A81198
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <TET>
A:Cross-references: UNIPROT:Q9K0V4; GB:AE002401; GB:AE002098; NID:97225669; PIDN:AAF40892
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0455
C:Superfamily: Bacillus conserved hypothetical protein ypsC

Query Match 83.8%; Score 31; DB 2; Length 380;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 48 YANLS 54

RESULT 7
A81833
conserved hypothetical protein NMA2030 [imported] - Neisseria meningitidis (strain Z2491
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: A81833
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
J.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: A81833
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <PAR>
A:Cross-references: UNIPROT:Q9R0W4; GB:AL162757; GB:AL157959; NID:97380371; PIDN:CAB85245
A:Experimental source: serogroup A, strain Z2491
C:Genetics:

A:Gene: NMA2030
C:Superfamily: Bacillus conserved hypothetical protein ypsC

Query Match 83.8%; Score 31; DB 2; Length 380;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
||:||||
DB 48 YANLHS 54

RESULT 8

AF0777
probable transcription regulator STY2390 [imported] - Salmonella enterica subsp. enteric

C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AF0777

R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A:Reference number: AB0502; WUID:21534947; PMID:11677608
A/Accession: AF0777

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD02540.1; PID:G16503401; GSPDB:GN00176
C:Genetics:

A:Gene: STY2390
C:Superfamily: probable transcription regulator ypsE

Query Match 81.1%; Score 30; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLHS 7
|||||
DB 94 SSNLHS 99

RESULT 9

AI2054
hypothetical protein all1991 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AI2054

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A:Reference number: AB1807; WUID:21595285; PMID:11759840
A/Accession: AI2054

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <RUR>

A:Cross-references: UNIPROT:Q8YV17; GB:BA000019; PIDN:BA873690.1; PID:G17131081; GSPDB:G A:Experimental source: strain PCC 7120
C:Genetics:

A:Gene: all1991

Query Match 81.1%; Score 30; DB 2; Length 290;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6
||:||||
DB 190 YSNLH 195

RESULT 10
T48439
probable RNA-binding protein - Arabidopsis thaliana

N:Alternate names: protein T32M21.30
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: T48439

R:Bevan, M.; Terry, N.; Ardiles, W.; Buysbaert, C.; Dasseville, R.; De Clerck, R.; De l ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24487
A/Accession: T48439

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-313 <BEV>

A:Cross-references: UNIPROT:Q9L282; EMBL:ALJ62875
A:Experimental source: cultivar Columbia; BAC clone T32M21

C:Genetics:
A:Map position: 5
A:Interons: 29/1; 108/3; 144/2; 209/1; 229/3; 261/3; 282/2
A:Note: T32M21.30

Query Match 81.1%; Score 30; DB 2; Length 313;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
||:||||
DB 197 YSQNVHS 203

RESULT 11

S72617

alcohol dehydrogenase homolog B11-4 [imported] - Neurospora crassa

N:Alternate names: protein B24M22.250
C:Species: Neurospora crassa

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: S72617; T51229

R:Brucher, J.J.P.; Eberle, J.; Kohler, W.; Kruff, V.; Radford, A.; Russo, V.E.A.
Mol. Gen. Genet. 252, 223-229, 1996

A:Title: b11-4, a gene that is rapidly induced by blue light, encodes a novel mitochondr A:Reference number: S72617; WUID:96439828; PMID:8842141
A/Accession: S72617

A:Molecule type: mRNA
A:Residues: 1-412 <BRU>

A:Cross-references: UNIPROT:Q92247; EMBL:X89499; NID:G1620434; PIDN:CAA61670.1; PID:G162 A:Experimental source: mycelium, strain Stc
A:Genetics: BRU1

R:Schulte, U.; Aign, V.; Hohenstein, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25286
A/Accession: T51229

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-412 <SCH>
A:Cross-references: EMBL:AL390354; PIDN:CAB99393.1; GSPDB:GN00116; NCSP:B24M22.250
A:Experimental source: strain OR74A

A:Genetics: SCH1
C:Genetics: <BRU1>

A:Gene: b11-4
A:Map position: 11

C:Genetics: <SCH1>
A:Gene: B24M22.250

A:Map position: 6
A:Interons: 67/3; 320/2

C:Function:
A:Description: may play a role as an (NAD+)-dependent alcohol dehydrogenase in mitochondr

C:Keywords: mitochondrion

Query Match 81.1%; Score 30; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 95;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSNLS 7
|||||
Db 240 SSNLS 245

RESULT 12

hypoetical protein [imported] - Arabidopsis thaliana

C86247

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: C86247

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:1130712

A/Accession: C86247

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-424 <STO>

A/Cross-references: UNIPROT:Q96XB7; GB:AE005172; NID:95734725; PIDN:AMD49990.1; GSPDB:GN

C/Genetics:

A/Map position: 1

Query Match 81.1%; Score 30; DB 2; Length 424;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLS 7
|||||

Db 277 SSNLS 282

RESULT 13

hypoetical protein R06B9.1 - Caenorhabditis elegans

T23954

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T23954

R/Baynes, C. submitted to the EMBL Data Library, December 1996

A/Reference number: Z19823

A/Accession: T23954

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1427 <WIL>

A/Cross-references: UNIPROT:O17981; EMBL:Z83237; PIDN:CA805786.1; GSPDB:GN00020; CESP:RD

A/Experimental source: Clone R06B9

C/Genetics:

A/Map position: 2

A/Introns: 62/2; 97/3; 156/1; 380/1

C/Superfamily: Caenorhabditis elegans hypoetical protein R06B9.1

Query Match 81.1%; Score 30; DB 2; Length 427;

Best Local Similarity 83.3%; Pred. No. 98;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
|||||

Db 77 YSSNLS 82

RESULT 14

P97296

UDP-N-acetylmutamate-alanine ligase [imported] - Clostridium acetobutylicum

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C/Accession: P97296

R/Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

U. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: P97296

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-458 <KUR>

A/Cross-references: UNIPROT:Q97889; GB:AE001437; PIDN:AAK81161.1; PID:915026298; GSPDB:GT

A/Experimental source: Clostridium acetobutylicum ATCC824

C/Genetics:

A/Map position: CAC3225

C/Superfamily: UDP-N-acetylmutamate-alanine ligase

Query Match 81.1%; Score 30; DB 2; Length 458;

Best Local Similarity 100.0%; Pred. No. 11e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLS 7
|||||

Db 417 SSNLS 422

RESULT 15

two component sensor kinase envZ [imported] - Agrobacterium tumefaciens (strain C58, Dupc

AF2847

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: AF2847

R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

er, Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E

ster, B.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AF2847

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-459 <KUR>

A/Cross-references: UNIPROT:Q8UDC0; GB:AE008688; PIDN:AML43196.1; PID:917740676; GSPDB:GT

A/Experimental source: strain C58 (dupont)

C/Genetics:

A/Map position: envZ

Query Match 81.1%; Score 30; DB 2; Length 459;

Best Local Similarity 83.3%; Pred. No. 11e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
|||||

Db 371 YSSNLS 376

RESULT 16

omulativity sensor protein envZ (envZ) rp426 [imported] - Agrobacterium tumefaciens (straj

E97624

C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C/Accession: E97624

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappae, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: E97624

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <KUR>
A:Cross-references: UNIPROT:Q8UDC0; GB:AE007869; PIDN:AAK87950.1; PID:G15157354; GSPDB:C
A:Gene: AGR_C4011
A:Map position: circular chromosome

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 459;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLMH 6
DB 371 YASNLMH 376

RESULT 17

AD2532
hypothetical protein alr7543 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCCT120b
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2532
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MWID:21595285; PMID:11759640
A:Accession: AD2532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <KUR>
A:Cross-references: UNIPROT:Q8ZSG7; GB:AP003602; PIDN:BAH77186.1; PID:G17134628; GSPDB:C
A:Experimental source: strain PCC 7120
A:Genetics:
A:Gene: alr7543
A:Genome: plasmid

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 472;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLMH 6
DB 170 YSTNLMH 175

RESULT 18

T17257
hypothetical protein DKFZP586P1422.1 - human
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17257
R:Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18722
A:Accession: T17257
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-816 <KOE>
A:Cross-references: UNIPROT:Q9UFR2; EMBL:AL117472
A:Experimental source: adult uterus, clone DKFZP586P1422
A:Genetics:
A:Note: DKFZP586P1422.1

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 816;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLMH 7
DB 492 YSSNLMH 498

RESULT 19

B83136
probable fimbrial biogenesis usher protein PA084 [imported] - Pseudomonas aeruginosa (str
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83136
R:Stover, C.K.; Pham, X.Q.; EWitt, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim,
., Loay, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MWID:20437337; PMID:10984043
A:Accession: B83136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-844 <STO>
A:Cross-references: UNIPROT:Q9HWU4; GB:AE004824; GB:AE004091; NID:G9950277; PIDN:AAG07473
A:Experimental source: strain PA01
A:Genetics:
A:Gene: PA084
C:Superfamily: outer membrane usher protein fimb

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 844;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLMH 6
DB 169 YSSNLMH 174

RESULT 20

GBECB
beta-galactosidase (EC 3.2.1.23) alpha chain - Escherichia coli (strain K-12)
N:Alternate names: beta-D-galactoside galactohydrolase; lactase; phospho-beta-D-galactosi
C:Species: Escherichia coli
C:Date: 30-Sep-1987 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A65096; A25751; S09206
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MWID:97426617; PMID:9278503
A:Accession: A65096
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1042 <BLAT>
A:Cross-references: UNIPROT:P06864; UNIPROT:Q47170; GB:AE000389; GB:U00096; NID:G1789451;
A:Experimental source: strain K-12, substrain MG1655
R:Stokes, H.W.; Betts, P.W.; Hall, B.G.
Mol. Biol. Evol. 2, 469-477, 1985
A:Title: Sequence of the ebgA gene of Escherichia coli: comparison with the lacZ gene.
A:Reference number: A93056; MWID:88216133; PMID:3939707
A:Accession: A25751
A:Molecule type: DNA
A:Residues: 80-476, 'R', 478-651, 'S', 653-660, 'P', 662-674, 'CRSWTPAKRS', 685-724, 'KCAVS', 730-'
A:Cross-references: GB:X02228; GB:M13700; GB:M13796; NID:G41311; PIDN:CAA26978.1; PID:G41
J. Biol. Chem. 258, 10204-10207, 1983
A:Title: The active site regions of lacZ and ebg beta-galactosidases are homologous.
A:Reference number: A92390; MWID:83290932; PMID:6111710
A:Contents: annotation; active site regions
R:Hall, B.G.; Betts, P.W.; Wootton, J.C.
Genetics 123, 635-648, 1989
A:Title: DNA sequence analysis of artificially evolved ebg enzyme and ebg repressor gene
A:Reference number: S09206; MWID:90128218; PMID:2515108
A:Accession: S09206
A:Molecule type: DNA
A:Residues: 13-476, 'R', 478-651, 'S', 653-660, 'P', 662-674, 'M', 780-1037, 'T', 1039-1042 <HAL>
A:Cross-references: EMBL:X52031; NID:G41307; PIDN:CAA36274.1; PID:G41309
C:Comment: The wild-type enzyme is an ineffective lactase. Two classes of point mutations

C/Genetics:
A:Gene: ebga
A:Map position: 68 min
C:Complex: homohexamer
C:Superfamily: beta-galactosidase
C:Keywords: glycosidase; hexamer; hydrolase; magnesium
F:113,415,461/Binding site: magnesium (Glu, His, Glu) #status predicted
F:461,502,524/Active site: Glu, Tyr, Glu #status predicted

Query Match 81.1%; Score 30; DB 1; Length 1042;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
Db 1032 FSTNLHS 1038

RESULT 21
E85968
evolved beta-D-galactosidase alpha subunit [imported] - Escherichia coli (strain O157:H7)
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: E85968
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimianta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1042 <STO>
A:Cross-references: UNIPROT:Q8XAM9; GB:AE005174; NID:912517660; PIDN:AAG58209.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A:Gene: ebga
C:Superfamily: beta-galactosidase

Query Match 81.1%; Score 30; DB 2; Length 1042;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
Db 1032 FSTNLHS 1038

RESULT 22
F91123
evolved beta-D-galactosidase alpha subunit [imported] - Escherichia coli (strain O157:H7)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: F91123
R:Haysashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kohata, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91123
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1042 <HAY>
A:Cross-references: UNIPROT:Q8XAM9; GB:BA000007; PIDN:BA837381.1; PID:G13363431; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A:Gene: EC63958
C:Superfamily: beta-galactosidase

Query Match 81.1%; Score 30; DB 2; Length 1042;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
Db 1032 FSTNLHS 1038

RESULT 23
H86557
polymorphic membrane protein B Family [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: H86557
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ish
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: H86557
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1723 <STO>
A:Cross-references: UNIPROT:Q9Z812; GB:BA000008; NID:G8978911; PIDN:BA98746.1; GSPDB:GN
A:Experimental source: strain J138
C/Genetics:
A:Gene: pmp_20

Query Match 81.1%; Score 30; DB 2; Length 1723;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLHS 7
:|||||
Db 105 SSNLHS 110

RESULT 24
E72067
polymorphic membrane protein B family - Chlamydia pneumoniae (strain CWL029)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: E72067
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72067
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1723 <ARN>
A:Cross-references: UNIPROT:Q9Z812; GB:AE001638; GB:AE001363; NID:94376819; PIDN:AAD1868
A:Experimental source: strain CWL029
C/Genetics:
A:Gene: pmp_20

Query Match 81.1%; Score 30; DB 2; Length 1723;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLHS 7
:|||||
Db 105 SSNLHS 110

RESULT 25
C81601
polymorphic membrane protein B/C family CP0212 [imported] - Chlamydia pneumoniae (str
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C/Accession: C81601
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberger, J.F.; White, O.; Hickey, F
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: C81601

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1732 <REA>
A:Cross-references: GB:AE002182; GB:AE002161; NID:G7189140; PIDN:AAF38082.1; PID:G718914
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0212

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 1732;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSSNLS 7
Db 114 SSNLS 119

RESULT 26

IG kappa chain V region (MOPC 173) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C:Accession: A01926

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-

A:Reference number: A01926; PMID:812696

A:Accession: A01926

A:Molecule type: protein

A:Residues: 1-108 <SCH>

A:Cross-references: UNIPROT:P01643

C:Comment: This chain was isolated from a myeloma protein.

C:Complex: An immunoglobulin heterodimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 16

C:Keywords: heterodimer

F:16-90/Domain: immunoglobulin homology <IMM>

F:23-88/Disulfide bonds: #status predicted

Query Match
Best Local Similarity 78.4%; Score 29; DB 1; Length 108;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 50 YTSLS 56

RESULT 27

IG kappa chain V region (Py69) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C:Accession: G38740

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-

A:Reference number: A38740; PMID:91177923; PMID:1706720

A:Accession: G38740

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A:Molecule type: mRNA

A:Residues: 1-111 <RUF>

A:Cross-references: UNIPROT:Q91WS9

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterodimer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 78.4%; Score 29; DB 2; Length 111;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 114 SSNLS 119

Db 53 YTSLS 59

RESULT 28

IG kappa chain V region (Py20) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C:Accession: A38740

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-

A:Reference number: A38740; PMID:91177923; PMID:1706720

A:Accession: A38740

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A:Molecule type: mRNA

A:Residues: 1-111 <RUF>

A:Cross-references: UNIPROT:Q91WS9

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterodimer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 78.4%; Score 29; DB 2; Length 111;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 53 YTSLS 59

RESULT 29

IG kappa chain V region (Py54) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C:Accession: E38740

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-

A:Reference number: A38740; PMID:91177923; PMID:1706720

A:Accession: E38740

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A:Molecule type: mRNA

A:Residues: 1-111 <RUF>

A:Cross-references: UNIPROT:Q91WS9

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterodimer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 78.4%; Score 29; DB 2; Length 111;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 53 YTSLS 59

RESULT 30

IG kappa chain V region (Py2) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C:Accession: G38740

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-

A:Reference number: A38740; PMID:91177923; PMID:1706720

A:Accession: G38740

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A:Molecule type: mRNA

A:Residues: 1-111 <RUF>

A:Cross-references: UNIPROT:Q91WS9
 C:Superfamily: immunoglobulin V region, immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 29; DB 2; Length 111;
 Best Local Similarity 71.4%; Pred. No. 38;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 ||:||||
 Db 53 YSSLSHS 59

RESULT 31
 T11242
 ribosomal protein S3, mitochondrial - red alga (Porphyra purpurea) mitochondrion
 C:Species: mitochondrion Porphyra purpurea
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T11242
 R:Burger, G.; Saint-Louis, D.; Gray, M.W.; Lang, B.F.
 submitted to the EMBL Data Library, December 1998
 A:Description: Complete sequence of the mitochondrial DNA of the red alga, Porphyra purp
 A:Reference number: Z17255
 A:Accession: T11242
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-227 <BUR>

A:Cross-references: UNIPROT:O99993; EMBL:AF114794; NID:g4106927; PID:g4106954; PIDN:AAD0
 C:Genetics:
 A:Gene: rps3
 A:Genome: mitochondrion
 C:Function:
 A:Pathway: protein biosynthesis
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 78.4%; Score 29; DB 2; Length 227;
 Best Local Similarity 71.4%; Pred. No. 82;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 ||:||||
 Db 205 YSSSLHT 211

RESULT 32
 G89567
 protein T08A9.2 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
 C:Accession: G89567
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MIMD:99059613; PMID:9851916
 A:Note: see webistes genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elg
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: G89567
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-241 <STO>
 A:Cross-references: GB:chr X; PIDN:AAA81419.1; PID:g1065500; GSPDB:GN00028; CESP:T08A9.2
 A:Note: similar to C. elegans protein C40H1.5
 C:Genetics:
 A:Gene: T08A9.2
 A:Map position: X

Query Match 78.4%; Score 29; DB 2; Length 243;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 6
 |||||

Db 150 YSSNPF 155

RESULT 33
 TWMSJA

transcription factor AP-1 - mouse
 N:Alternate names: fos-associated 39K protein; protein PEA1; transcription factor, TGACTC
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
 C:Accession: A31345; S04683; S04537

R: Ryder, K.; Nathans, D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 8464-8467, 1988
 A:Title: Induction of protooncogene c-jun by serum growth factors.
 A:Reference number: A31345; MIMD:89042204; PMID:3186736

A:Accession: A31345
 A:Molecule type: mRNA
 A:Residues: 1-334 <RYD>
 A:Cross-references: UNIPROT:P05627; GB:J04115; NID:g192577; PIDN:AAA37419.1; PID:g309169
 R:Jamph, W.W.; Wamsley, P.; Sabatone-Corsi, P.; Verma, I.M.
 Nature 334, 629-631, 1988
 A:Title: Induction of proto-oncogene JUN/AP-1 by serum and TPA.
 A:Reference number: S04683; MIMD:88302467; PMID:2457172

A:Accession: S04683
 A:Molecule type: mRNA
 A:Residues: 1-334 <LAM>
 A:Cross-references: EMBL:X12740; NID:g52762; PIDN:CAA31336.1; PID:g52763
 R:Ryseck, R.P.; Hiral, S.I.; Yaniv, M.; Bravo, R.
 Nature 334, 535-537, 1988
 A:Title: Transcriptional activation of c-jun during the G(0)/G(1) transition in mouse fib

A:Reference number: S04537; MIMD:88302446; PMID:3136397
 A:Molecule type: mRNA
 A:Molecule type: mRNA
 A:Residues: 1-182; 'C', 184-334 <RYS>
 A:Cross-references: EMBL:X12761; NID:g52758; PIDN:CAA31352.1; PID:g52759
 C:Genetics:
 A:Gene: jun-A
 C:Superfamily: jun transforming protein; fos/jun DNA-binding domain homology
 C:Keywords: DNA binding; leucine zipper; phosphoprotein; proto-oncogene; transcription fa
 F:550-990/Domain: fos/jun DNA-binding domain homology <FJD>
 F:283-111/Region: leucine zipper motif

Query Match 78.4%; Score 29; DB 1; Length 334;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 ||:||||
 Db 159 YSASLSHS 165

RESULT 34
 S12742
 transcription factor AP-1 - rat
 N:Alternate names: transforming protein (jun)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: S12742; S20028; A37381
 R:Kitabayashi, I.; Saka, F.; Gachelin, G.; Yokoyama, K.
 Nucleic Acids Res. 18, 3400, 1990
 A:Title: Nucleotide sequence of rat c-jun protooncogene.
 A:Reference number: S12742; MIMD:90287724; PMID:2113275
 A:Accession: S12742
 A:Molecule type: DNA
 A:Residues: 1-334 <KIT>
 A:Cross-references: UNIPROT:P17325; EMBL:X17215; NID:g57079; PIDN:CAA35084.1; PID:g57080
 R:Kitabayashi, I.; Kawakami, Z.; Chiu, R.; Ozawa, K.; Matsuo, T.; Toyoshima, S.; Umesor
 EMO J. 11, 167-175, 1992
 A:Title: Transcriptional regulation of the c-jun gene by retinoic acid and B1a during dif
 A:Reference number: S20028; MIMD:92155155; PMID:1310930
 A:Accession: S20028
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-334 <KIT>

A/Cross-references: EMBL:X17215; NID:g57079; PIDN:CAA35084.1; PID:g57080
R:Sakai, M.; Okuda, A.; Hatayama, I.; Sato, K.; Nishi, S.; Muramatsu, M.
Cancer Res. 49, 5633-5637, 1999
A/Title: Structure and expression of the rat c-jun messenger RNA: tissue distribution and
A/Reference number: A37381; MWID:90002916; PMID:2507134
A/Accession: A37381
A/Molecule type: mRNA
A/Residues: 1-334 <SAS>
A/Cross-references: GB:X17163; NID:g57819; PIDN:CAA35041.1; PID:g57820
C/Genetics:
A/Genes: jun
A/Function:
A/Description: transcription factor
C/Superfamily: jun transforming protein; fos/jun DNA-binding domain homology
C/Keywords: DNA binding; leucine zipper; nucleus; phosphoprotein; transcription factor;
F:250-290/Domain: Fos/jun DNA-binding domain homology <F0D>
F:283-311/Region: leucine zipper motif

Query Match 78.4%; Score 29; DB 2; Length 334;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 159 YSASLMS 165

RESULT 35

25192
Hypothetical protein T23G11.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R/Gardner, A.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19993
A/Accession: T23192
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-347 <ML>
A/Cross-references: UNIPROT:Q45811; EMBL:Z81130; PIDN:CAE03416.1; GSPDB:GN00019; CESP:T2
A/Experimental source: clone T23G11
C/Genetics:
A/Genes: CESP:T23G11.2
A/Map position: 1
A/Introns: 74/2; 128/3; 250/2

Query Match 78.4%; Score 29; DB 2; Length 347;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 151 YSKNLH 156

RESULT 36

738822
Hypothetical protein SPAC4F10.18 - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R/Connor, R.; Churcher, C.M.; Barrrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A/Reference number: Z21813
A/Accession: T38822
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-391 <CON>
A/Cross-references: UNIPROT:O36030; EMBL:Z298980; PIDN:CAB11721.1; GSPDB:GN00066; SPDB:SH
A/Experimental source: strain 97Zh-; cosmid c4F10
C/Genetics:
A/Genes: SPDB:SPAC4F10.18

A/Map position: 1
A/Introns: 9/2; 35/1
C/Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4F10.18

Query Match 78.4%; Score 29; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 81 YSENLS 86

RESULT 37

B69675
glucose-6-phosphate isomerase pgl - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
R/Accession: B69675
R/Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Ertter, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maquda, S.; Maue
Y, M.; Ogasawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A/Authors: Schleich, S.; Schroeter, R.; Scifone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akushi, M.; Tanakoshi, A.; Tanaka, T.; Terasura, P.; Tognoni, A.; Toso, V.; Uchiyama
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zamestin, E.; Yoshikawa, H.; Darchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A63580; MWID:98044033; PMID:9384377
A/Accession: B69675
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-451 <KUN>
A/Cross-references: UNIPROT:P80860; GB:Z29120; GB:AL009126; NID:g2635613; PIDN:CAB15124.3
A/Experimental source: strain 168
C/Genetics:
A/Genes: pgl
C/Superfamily: glucose-6-phosphate isomerase

Query Match 78.4%; Score 29; DB 2; Length 451;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 307 YSTDLS 313

RESULT 38

G96655
unknown protein 29405-27288 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R/Accession: G96655
R/Theologis, A.; Ecker, J.R.; Palm, C.D.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anzen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Martini
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MWID:21016719; PMID:11130712
A/Accession: G96655
A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-465 <STO>
A:Cross-references: UNIPROT:Q9CAN8; GB:AE005173; NID:G659844; PIDN:AAF18699.1; GSPDB:GN
C:Genetics:
A:Gene: F16M19.14
A:Map position: 1

Query Match 78.4%; Score 29; DB 2; Length 465;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6
Db 63 FSSNLH 68

RESULT 39
T33061
hypothetical protein F56C3.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33061
R:Stonking, T.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid F56C3.
A:Reference number: Z21276
A:Accession: T33061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: UNIPROT:O61758; EMBL:AF067214; PIDN:AACT7005.1; GSPDB:GN00028; CESP:
A:Experimental source: strain Bristol N2; clone F56C3
C:Genetics:
A:Gene: CESP:F56C3.2
A:Map position: X
A:Introns: 69/2; 144/3; 230/2; 446/3
C:Superfamily: Caenorhabditis elegans hypothetical protein F47H4.4

Query Match 78.4%; Score 29; DB 2; Length 516;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6
Db 257 YQSNLH 262

RESULT 40
F90407
molybdopterin biosynthesis protein (moea-2) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C:Accession: F90407
R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Regan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: F90407
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-550 <KUR>
A:Cross-references: UNIPROT:Q97W71; GB:AE006641; NID:G13815669; PIDN:AAK42517.1; GSPDB:G
C:Genetics:
A:Gene: moea-2
C:Superfamily: Molybdenum cofactor molybdenum incorporation protein MoeA with molybdate-

Db 208 YSSNLH 213
Search completed: December 17, 2004, 18:30:16
Job time : 3.75281 secs

Query Match 78.4%; Score 29; DB 2; Length 550;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:29:23 ; Search time 20.9213 Seconds
(without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-7
Perfect score: 37
Sequence: 1 YSSNLHS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	4780	2	Q8IE54 plasmodium
2	34	91.9	404	2	Q7RI06
3	34	91.9	468	1	SKIP MOUSE
4	34	91.9	468	2	Ash66112 mus muscu
5	34	91.9	642	2	Q9PC03 streptomyc
6	34	91.9	744	2	Q62788 rattus norv
7	33	89.2	219	2	Q94192 caenorhabd1
8	33	89.2	368	2	Q9CD01 laccococcus
9	33	89.2	391	2	Q8RR04 cytophaga s
10	33	89.2	470	2	Q845X4 cellulophag
11	33	89.2	474	2	Q9AJ10 marine cfb
12	33	89.2	474	2	Q9ET58 tenacibacul
13	33	89.2	474	2	Q9ETV9 cytophaga 1
14	33	89.2	474	2	Q9FIY8 tenacibacul
15	33	89.2	474	2	Q9FIY9 tenacibacul
16	33	89.2	474	2	Q9FIZ0 tenacibacul
17	33	89.2	474	2	Q9FAV1 psychrotlex
18	33	89.2	474	2	Q9FAV9 cytophaga 1
19	33	89.2	474	2	Q9FAW0 cytophaga 1
20	33	89.2	474	2	Q9FAW1 cytophaga 1
21	33	89.2	474	2	Q9FAW2 cytophaga 1
22	33	89.2	480	2	Q9FAW4 capnocytoph
23	33	89.2	817	2	Q7PK57 anopheles g
24	32	86.5	169	2	Q9B950 lycopersico
25	32	86.5	172	2	Q70Y33 lycopersico
26	32	86.5	172	2	CAD44274
27	32	86.5	325	2	Q43751 capsicum an
28	32	86.5	331	2	Q22124 caenorhabd1
29	32	86.5	478	2	Q8ES05 oceanobact1
30	32	86.5	480	2	Q6BBD4 arabidopsis
31	32	86.5	481	2	Q9FPE4 arabidopsis

32	32	86.5	485	2	Q96547 capsicum an
33	32	86.5	489	2	Q42872 lycopersico
34	32	86.5	500	2	Q93W20 nicotiana t
35	32	86.5	536	2	Q83Z58 mesoplasma
36	32	86.5	598	2	Q708M6 anopheles g
37	32	86.5	615	2	Q9RP84 acholeplasm
38	31	83.8	335	2	Q8RPN2 fusobacteri
39	31	83.8	347	2	Q9L9Q6 campylobact
40	31	83.8	347	2	Q9LAK4 campylobact
41	31	83.8	347	2	Q9F0N1 campylobact
42	31	83.8	347	2	Q938X8 campylobact
43	31	83.8	347	2	AAR82873 campyloba
44	31	83.8	380	2	Q9RM00 neisseria m
45	31	83.8	380	2	Q9KOV4 neisseria m

ALIGNMENTS

```

RESULT 1
ID Q8IE54 PRELIMINARY; PRT; 4780 AA.
AC Q8IE54;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein PF13_0148.
GN Name=PF13_0148;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrett B.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844509; CAD52412.1; -
DR Interpro: IPR008266; Tyr_pkinase AS.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 4780 AA; 575455 MW; 568F461B83657D44 CRC64;

QY 1 YSSNLHS 7
Db 1325 YSSNLHS 1331

Query Match 100.0%; Score 37; DB 2; Length 4780;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ID Q7RI06 PRELIMINARY; PRT; 404 AA.
AC Q7RI06;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Asparagine-rich protein.
GN Name=PY03561;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=17XNL;
RC PubMed=12368865;
RX Carlton J.M., Anguinoi S.V., Suh B.B., Kooij T.W., Perrea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalton S.T., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,

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RA Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.,
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite *Plasmodium yoelii yoelii*.";
 RT Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL:AB01001031; EMBL5290.1; -;
 SQ SEQUENCE 404 AA; 47311 MW; 79DFBACAF87ADC CRC64;
 QY
 Db 1 YSSNLS 7
 302 YSSNLS 308
 Query Match 91.9%; Score 34; DB 2; Length 404;
 Best Local Similarity 85.7%; Pred. No. 77;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 SKIP MOUSE STANDARD; PRT; 468 AA.
 ID SKIP MOUSE
 AC 08C5L6; 009040;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Skeletal muscle and kidney enriched inositol phosphatase
 DE (EC 3.1.3.56).
 GN Name=Skip; Synonyms=Pps;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97325785; PubMed=9182797;
 RA Hamilton B.A., Smith D.J., Mueller K.L., Kerrebrock A.W.,
 RA Bronson R.T., van Berkel V., Daly M.J., Kruglyak L., Reeve M.P.,
 RA Nemauser J.L., Hawkins T.L., Rubin E.M., Lander E.S.,
 RT "The vibrator mutation causes neurodegeneration via reduced expression
 RT of PTP alpha: positional complementation cloning and extragenic
 RT suppression.";
 RL Neuron 18:711-722(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1IS, and 1SS;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Caniffie J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.,
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=057BL/6J; TISSUE=Medulla oblongata, and Ovary;
 RX MEDLINE=22354683; PubMed=12456851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikiado I., Oato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojodori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kampin A., Matsuda H., Batalov S., Beisler K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbett L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravaei T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Virardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyman-Borja A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai U., Mizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 CC -1- FUNCTION: Inositol 5-phosphatase which acts on inositol 1,4,5-
 CC triphosphate, inositol 1,3,4,5-tetrakisphosphate,
 CC phosphatidylinositol 4,5-bisphosphate and phosphatidylinositol
 CC 3,4,5-trisphosphate. Has 6-fold higher affinity for
 CC phosphatidylinositol 4,5-bisphosphate than for inositol 1,4,5-
 CC triphosphate. May negatively regulate assembly of the actin
 CC cytoskeleton (By similarity).
 CC -1- CATALYTIC ACTIVITY: D-myo-inositol 1,4,5-trisphosphate + H(2)O =
 CC myo-inositol 1,4-bisphosphate + phosphate.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum. Following stimulation
 CC with EGF, translocates to membrane ruffles (By similarity).
 CC -1- SIMILARITY: Belongs to the inositol-1,4,5-trisphosphate 5-
 CC phosphatase type II family.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC -----
 DR EMBL: U96724; AAC53265.1; -;
 DR EMBL: U96726; AAC60757.1; -;
 DR EMBL: AF483522; AAL90796.1; -;
 DR EMBL: AF483523; AAL90797.1; -;
 DR EMBL: AK054436; BAC35778.1; -;
 DR EMBL: AK078104; BAC37126.1; -;
 DR HSSP: O43001; 119Z.
 DR WGD; MG1:1194899; Ppe.
 DR GO; GO:0005829; C:cytosol; ISS.
 DR GO; GO:0043005; C:neuronal cell projection; ISS.
 DR GO; GO:0016312; F:inositol triphosphate phosphatase activity; ISS.
 DR GO; GO:0046030; F:inositol triphosphate phosphatase activity; ISS.
 DR GO; GO:0042577; F:lipid phosphatase activity; ISS.
 DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; ISS.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPC.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPCC; 1.
 KW Endoplasmic reticulum, Hydrolyase.
 FT DOMAIN 34 337 Catalytic (Potential).
 FT DOMAIN 340 468 Required for ruffle localization.
 FT CONFLICT 329 329 D -> E (in Ref. 3; F2E1CA370B978A1 CRC64;
 SQ SEQUENCE 468 AA; 54158 MW; F2E1CA370B978A1 CRC64;
 QY
 Db 1 YSSNLS 7
 434 YSSNLS 440
 Query Match 91.9%; Score 34; DB 1; Length 468;
 Best Local Similarity 85.7%; Pred. No. 91;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 4
 AAH66112 PRELIMINARY; PRT; 468 AA.
 ID AAH66112
 AC AAH66112;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)

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DT 14-APR-2004 (TrEMBLrel. 27, last sequence update)
DE 14-APR-2004 (TrEMBLrel. 27, last annotation update)
DE Pps protein.
GN Pps.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=23188257; PubMed=12477932;
RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalske U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066112; AAB6112.1; -.
SQ SEQUENCE 468 AA; 5418 MW; F2E1CA370B97A0A1 CRC64;

Query Match 91.9%; Score 34; DB 2; Length 468;
Best Local Similarity 85.7%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 434 YSSNLS 440

RESULT 5
O9FC03 PRELIMINARY; PRT; 642 AA.
AC O9FC03;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Purative secreted amidase.
GN OrderedAccession=SC07179; ORFNames=SC8A11.07c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=1200953; DOI=10.1038/41741a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Mowbray S.,
RA Huang C.-H., Kleiser I., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

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RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)";
RL Nature 417:141-147(2002).
DR EMBL; AL939130; CAC01579.1; -.
DR HSSP; P82974; 1J3G.
DR GO; GO:008745; F:N-acetyl[muramoyl]-L-alanine amidase activity; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002502; Amidase_2.
DR Pfam; PF01510; Amidase_2; 1.
DR SMART; SM00644; Ami_2; 1.
KW Complete proteome.
SQ SEQUENCE 642 AA; 67149 MW; 4659E442C31A033 CRC64;

Query Match 91.9%; Score 34; DB 2; Length 642;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 323 YSSNLS 329

RESULT 6
O62788 PRELIMINARY; PRT; 744 AA.
AC O62788;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Cys2/His2 zinc finger protein.
GN Name=CXK2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96033674; PubMed=7595478;
RA Post U., Thiesen H.J., Colello R.J., Schwab M.E.;
RT "A new Cys2/His2 zinc finger gene, rXK2, is expressed in
RT differentiated rat oligodendrocytes and encodes a protein with a
RT functional repressor domain."
RL J. Neurochem. 65:1955-1966(1995).
DR EMBL; U27186; AAB60512.1; -.
DR HSSP; P25490; 1ZNM.
DR GO; GO:005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1.
DR DR Pfam; PF00096; zF_C2H2; 19.
DR ProDom; PD000003; Znf_C2H2; 17.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; ZNF_C2H2; 19.
DR PROSITE; PS50805; KRAB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 17.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 17.
SQ SEQUENCE 744 AA; 85421 MW; 02EDA246E4EAOFS CRC64;

Query Match 91.9%; Score 34; DB 2; Length 744;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 501 YSSNLS 507

RESULT 7

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Q94192
ID Q94192 PRELIMINARY; PRT; 219 AA.
AC Q94192;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein F22H10.6.
GN ORFNames=F22H10.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Hawkins J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, J070845; AAB09103.1; -.
DR PIR, T30122; T30122.
KW WormPeP; F22H10.6; CE09575.
DR Hypothetical protein.
SQ SEQUENCE 219 AA; 25258 MW; 2091CC121B35FDA CRC64;
Query Match 89.2%; Score 33; DB 2; Length 219;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLS 7
DB 22 FSSNLS 28
RESULT 8
Q9CDQ1
ID Q9CDQ1 PRELIMINARY; PRT; 368 AA.
AC Q9CDQ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein YweB.
GN Name=YweB; OrderedlocusNames=ll2167;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxId=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ll1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Winkler P., Manger S., Jallion O., Malame K.,
RA Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis ll1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL, AB006445; AAK06265.1; -.
DR PIR, G86895; G86895.

KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 368 AA; 41726 MW; C1243C3B9F140DD CRC64;
Query Match 89.2%; Score 33; DB 2; Length 368;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLS 7
DB 121 FSSNLS 127
RESULT 9
Q8RR04
ID Q8RR04 PRELIMINARY; PRT; 391 AA.
AC Q8RR04;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA gyrase subunit B (Ec 5.99.1.3) (Fragment).
GN Name=gyrB;
OS Cytophaga sp. T-588.
OC Bacteria; Bacteroidetes; Sphingobacteriales; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxId=173740;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22431356; PubMed=12542710;
RA Matsuo Y., Suzuki M., Kasei H., Shizuri Y., Harayama S.;
RT "Isolation and phylogenetic characterization of bacteria capable of
RT inducing differentiation in the green alga Monostroma oxyspermum.";
RL Environ. Microbiol. 5:25-35(2003).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL, AB073038; BAB88340.1; -.
DR HSSP; P06982; 1A76.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0018853; F:isomerase activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR001241; DNA_topoisom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c1.
DR PRINTS; PR00418; TP12FAMILY.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 391
SQ SEQUENCE 391 AA; 43486 MW; 0C5E029383468759 CRC64;
Query Match 89.2%; Score 33; DB 2; Length 391;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSSNLS 7
DB 158 YSENLS 164
RESULT 10
O845X4
ID O845X4 PRELIMINARY; PRT; 470 AA.
AC O845X4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cellulophaga fucicola.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxId=76595;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=LMG18536;
RX MEDLINE=22431356; PubMed=12542710;
RA Matsuo Y., Suzuki M., Kaebi H., Shizuri Y., Harayama S.;
RT Isolation and phylogenetic characterization of bacteria capable of
RT inducing differentiation in the green alga *Monostroma oxyspermum*.";
RL Environ. Microbiol. 5:25-35(2003).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (by similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL, AB071140; F:ATP binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB_1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 470 470 1
SQ SEQUENCE 470 AA; 52527 MW; DF6BAE2EFD21A7D6 CRC64;
Query Match 89.2%; Score 33; DB 2; Length 470;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSSNLS 7
DB 165 YESNLS 171
RESULT 11
Q9AJIO PRELIMINARY; PRT; 474 AA.
AC Q9AJIO;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS marine CFB-group bacterium MBIC04478.
OC Bacteria; Bacteroidetes.
OX NCBI_TaxId=135558;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MBIC4478;
RX Suzuki M., Takeda T., Harayama S., Yamamoto S.;
RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded

CC DNA rings, including catenanes and knotted rings (by similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL, AB047186; BAB40409.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB_1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 474 474 1
SQ SEQUENCE 474 AA; 52920 MW; 1E1E631B9CEDFCC2 CRC64;
Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSSNLS 7
DB 164 YESNLS 170
RESULT 12
Q9ETS8 PRELIMINARY; PRT; 474 AA.
AC Q9ETS8;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Tenacibaculum ovoliticum.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Tenacibaculum.
OX NCBI_TaxId=104270;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IFO15992, and IAM14318;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovoliticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylophilum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (by similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL, AB034231; BAB12489.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.

DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PR0204; DNA_gyraseB; 1.
DR Pfam; PR02518; HATPase_c; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 53026 MW; 8AEFA02A6E986E3 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7
Db 164 YSENLHS 170

RESULT 13
Q9ETV9 PRELIMINARY; PRT; 474 AA.
AC Q9ETV9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
NCBI_TaxId=979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBIC1544, and IF016022;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Hareyama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov.", and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
amylolyticum sp. nov.";
RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
RL -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
stranded DNA in an ATP-dependent manner and also catalyzes the
interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034215; BAB12476.1; -.
DR EMBL; AB034215; BAB12473.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA modification; IEA.
DR GO; GO:0006304; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.

DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 53160 MW; 792A989704BA3027 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7
Db 164 YSENLHS 170

RESULT 14
Q9F1Y8 PRELIMINARY; PRT; 474 AA.
AC Q9F1Y8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Tenacibaculum ovolyticum.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Tenacibaculum.
NCBI_TaxId=104270;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO15993;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Hareyama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov.", and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
amylolyticum sp. nov.";
RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
RL -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
stranded DNA in an ATP-dependent manner and also catalyzes the
interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034232; BAB12490.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; F:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 53068 MW; 7FEFA02A6E986F9 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7

Db 164 YSENLS 170

RESULT 15

ID 09F1Y9 PRELIMINARY; PRT; 474 AA.

AC 09F1Y9; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE DNA gyrase B subunit (Fragment).

GN Name=gyrB;

OS Tenacibaculum maritimum.

OC Bacteria; Bacteroidetes; Flavobacteriales; Flavobacteriaceae; Tenacibaculum.

CC NCBI_TaxID=107401;

CC [1] SEQUENCE FROM N.A.

CC STRAIN=ATCC43398;

CC MEDLINE=2147783; PubMed=11594591;

CC Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;

CC "Phylogenetic analysis and taxonomic study of marine Cytophaga-like bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov.", and description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum amylolyticum sp. nov.;"

CC Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).

CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings (By similarity).

CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

CC EMBL; AB034228; BAB12486.1; -.

CC DR GO; GO:0005524; F:ATP binding; IEA.

CC DR GO; GO:0003677; F:DNA binding; IEA.

CC DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.

CC DR GO; GO:0006304; P:DNA modification; IEA.

CC DR GO; GO:0006265; P:DNA topological change; IEA.

CC DR InterPro; IPR003594; ATPbind_ATPase.

CC DR InterPro; IPR011558; DNA_gyrase_B.

CC DR InterPro; IPR001241; DNA_topoisom.

CC DR InterPro; IPR006171; Toprim_dom.

CC DR Pfam; PF00204; DNA_gyraseB_1.

CC DR Pfam; PF02518; HATase_C_1.

CC DR Pfam; PF01751; Toprim_1.

CC DR PRINTS; PR00418; TP12FAMILY.

CC DR Prodom; PD149633; DNA_gyrase_B_1.

CC DR SMART; SM00433; TOP2c_1.

CC DR PROSITE; PS00177; TOPOISOMERASE_II_1.

CC KM ATP-binding; Isomerase; Topoisomerase.

CC FT NON_TER 1

CC FT TER 474

CC SQ SEQUENCE 474 AA; 52888 MW; 47DIF2DB02B996E CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;

Best Local Similarity 85.7%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSENLS 7

Db 164 YSENLS 170

RESULT 16

ID 09F1Z0 PRELIMINARY; PRT; 474 AA.

AC 09F1Z0; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE DNA gyrase B subunit (Fragment).

GN Name=gyrB;

OS Tenacibaculum maritimum.

OC Bacteria; Bacteroidetes; Flavobacteriales; Flavobacteriaceae; Tenacibaculum.

CC NCBI_TaxID=107401;

CC [1] SEQUENCE FROM N.A.

CC STRAIN=JFO16015;

CC MEDLINE=2147783; PubMed=11594591;

CC Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;

CC "Phylogenetic analysis and taxonomic study of marine Cytophaga-like bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov.", and description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum amylolyticum sp. nov.;"

CC RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).

CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings (By similarity).

CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

CC EMBL; AB034228; BAB12486.1; -.

CC DR GO; GO:0005524; F:ATP binding; IEA.

CC DR GO; GO:0003677; F:DNA binding; IEA.

CC DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.

CC DR GO; GO:0006304; P:DNA modification; IEA.

CC DR GO; GO:0006265; P:DNA topological change; IEA.

CC DR InterPro; IPR003594; ATPbind_ATPase.

CC DR InterPro; IPR011558; DNA_gyrase_B.

CC DR InterPro; IPR001241; DNA_topoisom.

CC DR InterPro; IPR006171; Toprim_dom.

CC DR Pfam; PF00204; DNA_gyraseB_1.

CC DR Pfam; PF02518; HATase_C_1.

CC DR Pfam; PF01751; Toprim_1.

CC DR PRINTS; PR00418; TP12FAMILY.

CC DR Prodom; PD149633; DNA_gyrase_B_1.

CC DR SMART; SM00433; TOP2c_1.

CC DR PROSITE; PS00177; TOPOISOMERASE_II_1.

CC KM ATP-binding; Isomerase; Topoisomerase.

CC FT NON_TER 1

CC FT TER 474

CC SQ SEQUENCE 474 AA; 52960 MW; 4D738B7455D49FA8 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;

Best Local Similarity 85.7%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSENLS 7

Db 164 YSENLS 170

RESULT 17

ID 09FAV1 PRELIMINARY; PRT; 474 AA.

AC 09FAV1; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE DNA gyrase B subunit (Fragment).

GN Name=gyrB;

OS Psychroflexus gondwanensis.

OC Bacteria; Bacteroidetes; Flavobacteriales; Flavobacteriaceae; Psychroflexus.

CC NCBI_TaxID=251;

CC [1] SEQUENCE FROM N.A.

CC STRAIN=DSM5423;

CC MEDLINE=2147783; PubMed=11594591;

CC Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;

RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -I- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -I- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034216; BAB12484.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 474
FT NON_TER 1 474
SQ SEQUENCE 474 AA; 53686 MW; 417E2D2C08DFDB CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 YSSNLHS 7
|||
Db 164 YSENLS 170

RESULT 18
O9FAV9 PRELIMINARY; PRT; 474 AA.
ID O9FAV9;
AC O9FAV9; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name-gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO15986;
RX MEDLINE=2147783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -I- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining

CC of double-stranded DNA.
CC -I- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034217; BAB12475.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 474
FT NON_TER 1 474
SQ SEQUENCE 474 AA; 53133 MW; E1B3FE15802A948B CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 YSSNLHS 7
|||
Db 164 YSENLS 170

RESULT 19
O9FAW0 PRELIMINARY; PRT; 474 AA.
ID O9FAW0;
AC O9FAW0; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name-gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAM14306;
RX MEDLINE=2147783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -I- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -I- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034216; BAB12474.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.

DR InterPro; IPR006171; Toprim_dom.
 DR Pfam; PF00204; DNA_gyraseb; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF01751; Toprim_1.
 DR PRINTS; PR00418; TP12FAMILY.
 DR ProDom; PD149633; DNA_gyrase_B; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
 DR ATP-binding; Isomerase; Topoisomerase.
 FT NON_TER 1 1
 FT SEQUENCE 474 AA; 53147 MW; 2601AA18DCDC7E CRC64;
 SQ
 Query Match 89.2%; Score 33; DB 2; Length 474;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YSSNLS 7
 Db 164 YSENLS 170
 RESULT 20
 Q9PAM1 PRELIMINARY; PRT; 474 AA.
 ID Q9PAM1;
 AC Q9PAM1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DNA gyrase B subunit (Fragment).
 GN Name=gyrB;
 OS Cytophaga lytica.
 OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
 OC Flavobacteriaceae; Cellulophaga.
 NCBI_Taxid=979;
 RX MEDLINE=2147783; PubMed=11594591;
 RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
 RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
 RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
 RT maritimum comb. nov. and Tenacibaculum ovoidelicum comb. nov., and
 RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
 RT amylolyticum sp. nov.";
 RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
 CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
 CC stranded DNA in an ATP-dependent manner and also catalyzes the
 CC interconversion of other topological isomers of double-stranded
 CC DNA rings, including catenanes and knotted rings (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 CC EMBL; AB034214; BAB12472.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
 DR GO; GO:0006304; F:DNA modification; IEA.
 DR GO; GO:0006265; F:DNA topological change; IEA.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR011558; DNA_gyrase_B.
 DR InterPro; IPR001241; DNA_topoisom.
 DR InterPro; IPR006171; Toprim_dom.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF01751; Toprim_1.
 DR PRINTS; PR00418; TP12FAMILY.
 DR ProDom; PD149633; DNA_gyrase_B; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
 DR ATP-binding; Isomerase; Topoisomerase.
 FT NON_TER 1 1
 FT SEQUENCE 474 AA; 53119 MW; 38D059D7E0FE1F93 CRC64;
 SQ

SQ SEQUENCE 474 AA; 53001 MW; 1F874F9A8626182D CRC64;
 Query Match 89.2%; Score 33; DB 2; Length 474;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YSSNLS 7
 Db 164 YSENLS 170
 RESULT 21
 Q9PAM2 PRELIMINARY; PRT; 474 AA.
 ID Q9PAM2;
 AC Q9PAM2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DNA gyrase B subunit (Fragment).
 GN Name=gyrB;
 OS Cytophaga lytica.
 OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
 OC Flavobacteriaceae; Cellulophaga.
 NCBI_Taxid=979;
 RX MEDLINE=2147783; PubMed=11594591;
 RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
 RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
 RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
 RT maritimum comb. nov. and Tenacibaculum ovoidelicum comb. nov., and
 RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
 RT amylolyticum sp. nov.";
 RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
 CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
 CC stranded DNA in an ATP-dependent manner and also catalyzes the
 CC interconversion of other topological isomers of double-stranded
 CC DNA rings, including catenanes and knotted rings (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 CC EMBL; AB034213; BAB12471.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
 DR GO; GO:0006304; F:DNA modification; IEA.
 DR GO; GO:0006265; F:DNA topological change; IEA.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR011558; DNA_gyrase_B.
 DR InterPro; IPR001241; DNA_topoisom.
 DR InterPro; IPR006171; Toprim_dom.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF01751; Toprim_1.
 DR PRINTS; PR00418; TP12FAMILY.
 DR ProDom; PD149633; DNA_gyrase_B; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
 DR ATP-binding; Isomerase; Topoisomerase.
 FT NON_TER 1 1
 FT SEQUENCE 474 AA; 53119 MW; 38D059D7E0FE1F93 CRC64;
 SQ
 Query Match 89.2%; Score 33; DB 2; Length 474;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YSSNLS 7
 Db 164 YSENLS 170

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RESULT 22
Q9FAW4 PRELIMINARY; PRT; 480 AA.
ID Q9FAW4;
AC Q9FAW4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Capnocytophaga canimorsus.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
NC NCBITaxId=28188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC35979;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayana S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovoidicum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylophilum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -I- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (by similarity).
CC -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -I- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034211; BAB12469.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; F:DNA modification; IEA.
DR GO; GO:0006265; F:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB_1.
DR Pfam; PF02518; HATPase_c_1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD149633; DNA_gyrase_B_1.
DR SMART; SM00433; TOP2c_1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 480
SQ SEQUENCE 480 AA; 53889 MW; 5F1F48BD18CEE052 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 480;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 164 YSSNLS 170

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OC Neoptera; Endopterygota; Diptera; Nematocera; Culioidae; Anopheles.
OX NCBITaxId=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA01008987; EAA01793.1; -.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 817 AA; 87412 MW; F898FB95B8B2995 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 589 YSSNLS 594

RESULT 24
Q9S950 PRELIMINARY; PRT; 169 AA.
ID Q9S950;
AC Q9S950;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CEL2-CELLULOSE 2 (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
NC NCBITaxId=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96291721; PubMed=8754682;
RA del Campillo E., Bennett A.B.;
RT "Pedicle breakstrength and cellulase gene expression during tomato
RT flower abscission.";
RL Plant Physiol. 111:813-820(1996).
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR01701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6np.
DR Pfam; PF00759; Glyco_hydro_9; 1.
FT NON_TER 1
FT NON_TER 169
FT NON_TER 169
SQ SEQUENCE 169 AA; 18674 MW; CE8AB3AC5637C481 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 169;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 143 YSSNLS 149

RESULT 25
Q70Y33 PRELIMINARY; PRT; 172 AA.
ID Q70Y33;
AC Q70Y33;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative endo-1,4,-beta-glucanase (Fragment).
GN Name=cel;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

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OC lamidae; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=fruit;
RA Saispress G.V.S., Lalitha A.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ505749; CAD44274.1; -
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF00759; Glyco_hydro_9; 1.
FT NON_TER 1
FT NON_TER 172
SQ SEQUENCE 172 AA; 19004 MW; F8584877ABEB83F9 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 172;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 144 YSSLSHS 150

RESULT 26
CAD44274 PRELIMINARY; PRT; 172 AA.
AC CAD44274;
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE Putative endo-1,4,-beta-glucanase (Fragment).
GN CEL.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamidae; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Arka vikas; TISSUE=fruit;
RA Saispress G.V.S., Lalitha A.;
RT "Isolation, cloning and characterization of endo-1,4,-beta-glucanase
RT gene from ripening tomato fruit (Lycopersicon esculentum cv. Arka
RT vikas)";
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ505749; CAD44274.1; -
FT NON_TER 1
FT NON_TER 172
SQ SEQUENCE 172 AA; 19004 MW; F8584877ABEB83F9 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 172;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 144 YSSLSHS 150

RESULT 27
O43751 PRELIMINARY; PRT; 325 AA.
AC O43751;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Cellulase (EC 3.2.1.4) (Fragment).
GN Name=cc3;
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamidae; Solanales; Solanaceae; Capsicum.

OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=leaf abscission zones;
RA Ferrarese L., Trainotti L., Morelto P., De Laureto P.P., Rascto N.,
RA Casadaro G.;
RT "Differential ethylene-inducible expression of cellulase in pepper
RT plants";
RL Mol. Biol. 29:735-747(1995).
DR EMBL; X83711; CA58686.1; -
DR PIR; S61447; S61447.
DR GO; GO:000810; P:cellulase activity, IEA.
DR GO; GO:0005975; P:carbohydrate metabolism, IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF00759; Glyco_hydro_9; 1.
KW Glycosidase; Hydrolyase.
FT NON_TER 1
FT NON_TER 325
SQ SEQUENCE 325 AA; 36087 MW; CE2040A6C7B17937 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 325;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 144 YSSLSHS 150

RESULT 28
O22124 PRELIMINARY; PRT; 331 AA.
AC O22124;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE C. elegans SRU-48 protein.
GN Name=sru-48;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Watson R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41272; AA82450.2; -
DR PIR; T29924; T29924.
DR InterPro; IPR003839; DUF215.
DR Pfam; PF02688; DUF215; 1.
SQ SEQUENCE 331 AA; 37829 MW; 7FC40A485B9F837 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 331;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 144 YSSLSHS 150

Db 325 YRSNLS 331

RESULT 29

Q8ES05 PRELIMINARY; PRT; 478 AA.

AC Q8ES05; 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)

DE Prollyl-cRNA synthetase.

GN Ordered locus Names=O80566;

OS Oceanobacillus thelyensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.

OX NCBI_TaxID=182710;

RN [1] _____

RP SEQUENCE FROM N.A.

RC STRAIN=HTE831;

RX MEDLINE=22220767; PubMed=1235376;

RA Takami H., Takaki Y., Uchiyama I.;

RT Genome sequence of Oceanobacillus thelyensis isolated from the Iheya

RT Ridge and its unexpected adaptive capabilities to extreme

RT environments.";

RL Nucleic Acids Res. 30:3927-3935(2002).

CC -1. SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

DR EMBL; AB004594; BAC12522.1; -.

DR HSSP; Q93N97; 1HC7.

DR GO; GO:0005737; Cytoplasm; IEA.

DR GO; GO:0005524; P:ATP binding; IEA.

DR GO; GO:0004827; P:proline-tRNA ligase activity; IEA.

DR GO; GO:0006433; P:prolyl-tRNA aminoacylation; IEA.

DR GO; GO:0006412; P:protein biosynthesis; IEA.

DR InterPro; IPR004154; HGRP anticodon.

DR InterPro; IPR002314; tRNA-synt 2b.

DR InterPro; IPR006195; tRNA_ligase_II.

DR Pfam; PF03129; HGRP-anticodon; 1.

DR Pfam; PF00587; tRNA-synt 2b; 1.

DR PRINTS; PRO1046; TRNASYNTHPRO.

DR TIGRFAMs; TIGR00408; pros_fam_1; 1.

DR PROSITE; PS00862; AA-TRNA_LIGASE_II; 1.

KW Aminoacyl-tRNA synthetase; Complete proteome.

SQ SEQUENCE 478 AA; 54750 MW; 5E37D353928D80 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 478;

Best Local Similarity 71.4%; Pred. No. 2.5e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSNLS 7

Db 125 YRSNLS 131

RESULT 30

Q6DBD4 PRELIMINARY; PRT; 480 AA.

ID Q6DBD4; 01-OCT-2004 (TrEMBLrel. 28, Created)

DT 01-OCT-2004 (TrEMBLrel. 28, last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 28, last annotation update)

DE At5g16410.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC euroside II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1] _____

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Shin P., Ecker J.R.;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL; E010508; AAT71960.1; -.

SQ SEQUENCE 480 AA; 53687 MW; 4984BF0029021C5A CRC64;

Query Match 86.5%; Score 32; DB 2; Length 480;

Best Local Similarity 85.7%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSNLS 7

Db 5 YRSNLS 11

RESULT 31

Q9PFE4 PRELIMINARY; PRT; 481 AA.

ID Q9PFE4; 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)

DE Similarity to N-hydroxycinnamoyl/benzoyltransferase.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC euroside II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1] _____

RP SEQUENCE FROM N.A.

RX MEDLINE=97471969; PubMed=9330910;

RX Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,

RA Miyajima N., Tabata S.;

RT Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence

RT features of the 1.6 Mb regions covered by twenty physically assigned

RL clones.";

RL DNA Res. 4:215-230(1997).

DR EMBL; AB005242; BAB09608.1; -.

DR GO; GO:0016740; P:transferase activity; IEA.

DR InterPro; IPR003480; Transferase.

DR Pfam; PF02458; Transferase; 1.

KW Transferase.

SQ SEQUENCE 481 AA; 53819 MW; B7991EF5CA339B7 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 481;

Best Local Similarity 85.7%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSNLS 7

Db 6 YRSNLS 12

RESULT 32

Q96547 PRELIMINARY; PRT; 485 AA.

ID Q96547; 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)

DE Cellulase (Endo-beta-1,4-glucanase) (EC 3.2.1.4).

GN Name=ccl3;

OS Capsicum annuum (Bell pepper).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamiales; Solanales; Solanaceae; Capsicum.

OX NCBI_TaxID=4072;

RN [1] _____

RP SEQUENCE FROM N.A.

RC TISSUE=Abscission zone;

RA Traenkle L., Ferrarese L., Casadoro G.;

RT "Different endo-beta-1,4-glucanases are expressed during abscission

RT and fruit ripening in pepper and peach plants.";

RL (in) Kanelis A.K., Chang C., Kende and Giersen D. (eds.);

RL BIOLOGY AND BIOTECHNOLOGY OF THE PLANT HORMONE ETHYLENE, pp.191-196,

RL Kluwer Academic Publishers, Dordrecht (1998).

RN [2] _____

RP SEQUENCE FROM N.A.


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RC TISSUE=Abcission zone;
RA Casadoro G.;
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97189; CAA65827.1; -.
DR HSSP; 077044; 1KS8..
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6np.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KM Glycosidase; Hydrolase.
SQ SEQUENCE 485 AA; 53631 MW; A8BCCB32E3FFA18A CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 485;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 213 YSSSLHS 219

RESULT 33
Q42872 PRELIMINARY; PRT; 489 AA.
ID Q42872;
AC Q42872;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endo-1,4-beta-glucanase precursor (EC 3.2.1.4).
GN Name=Cel2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Caslemart; TISSUE=Pericarp;
RX MEDLINE=95086382; PubMed=7994180;
RA Laabrook C.C., Gonzalez-Bosch C., Bennett A.B.;
RT "Two divergent endo-beta-1,4-glucanase genes exhibit overlapping
RT expression in ripening fruit and abscising flowers.";
RL Plant Cell 6:1485-1493(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Caslemart; TISSUE=Pericarp;
RA Brumwell D.A., Laabrook C.C., Bennett A.B.;
RT "Plant endo-1,4-beta-D-glucanases: structure, properties, and
RT physiological function.";
RL ACS Symp. Ser. 566:100-129(1994).
DR EMBL; U13055; AAA69909.1; -.
DR PIR; T06350; T06350.
DR HSSP; 077044; 1KS8.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6np.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KM Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 489 endo-1,4-beta-glucanase.
SQ SEQUENCE 489 AA; 54118 MW; FFADA8C4675F685F CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 489;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 216 YSSSLHS 222

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RESULT 34 ...
Q93WZ0 PRELIMINARY; PRT; 500 AA.
ID Q93WZ0;
AC Q93WZ0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endo-beta-1,4-glucanase precursor (EC 3.2.1.4).
GN Name=Cel2;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nematode-Infected roots;
RX MEDLINE=21480065; PubMed=11595799;
RA Goellner M., Wang X., Davis B.L.;
RT "Endo-beta-1,4-glucanase expression in compatible plant-nematode
RT interactions.";
RL Plant Cell 13:2241-2255(2001).
DR EMBL; AF362948; AAL30453.1; -.
DR HSSP; 077044; 1KS8.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6np.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KM Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 35 Potential.
FT CHAIN 36 500 endo-beta-1,4-glucanase.
SQ SEQUENCE 500 AA; 55075 MW; 28B48D421165798 CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 500;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 228 YSSSLHS 234

RESULT 35
Q83Z58 PRELIMINARY; PRT; 536 AA.
ID Q83Z58;
AC Q83Z58;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA gyrase subunit B (Fragment).
GN Name=gyrB;
OS Bacterioides plebeius.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmatales; Mesoplasma.
OX NCBI_TaxID=228419;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49582;
RA Knight T.F. Jr., Lawhorn I., Gasparich G.E.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY; Belongs to the type II topoisomerase family.
DR EMBL; AY257486; AAP13529.1; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003916; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.

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DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomI.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
FT NON_TER
SQ SEQUENCE 536 AA; 60040 MW; E302FC23AE9C5D09 CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 536;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 235 YSSNLS 241

RESULT 36
Q708M6 PRELIMINARY; PRT; 598 AA.
AC Q708M6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE AGCP15336 (Fragment).
GN Name=agCG49789; ORFNames=ENSAMCG0000018304;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OK NCBI_TaxId=180454;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008944; EXA10074.1; -.
DR GO; GO:0042765; C:GPI-anchor transamidase complex; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR007245; Gp116.
DR Pfam; PF04113; Gp116; 1.
FT NON_TER
SQ SEQUENCE 598 AA; 67546 MW; 260B7B630D02C13A CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 598;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 216 YSSNLS 222

RESULT 37
Q9RP84 PRELIMINARY; PRT; 615 AA.
AC Q9RP84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA gyrase beta subunit.
GN Name=gyrB;
RA Achotepiasma laidlawi.

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OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxId=2148;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=PG-8B;
RX MEDLINE=20242229; PubMed=10779957;
RA Taganov K.D., Gushchin A.E., Akopian T.A., Oparina N.Iu,
RA Abramycheva N.Iu, Govorun V.M.;
RT "Analysis of genes, coding for DNA gyrase from the mycoplasma
RT Acholeplasma laidlawi PG-8B.";
RL Mol. Biol. (Mosk.) 34:292-299(2000).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AF167102; AAD52967.1; -.
DR HSSP; P06982; 1A56.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0003304; P:DNA modification; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR002288; DNA_gyraseB_C.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomI.
DR InterPro; IPR011557; Gyrase.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF00986; DNA_gyraseB_C; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00433; TOP2c; 1.
DR TIGRFAMs; TIGR01059; gyrB; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
SQ SEQUENCE 615 AA; 68900 MW; 4D9962C35BAB73FE CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 615;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 267 YSSNLS 273

RESULT 38
Q8RFN2 PRELIMINARY; PRT; 335 AA.
AC Q8RFN2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter ATP-binding protein.
GN OrderedocusNames=FN0660;
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxId=76856;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=2186394; PubMed=11889109;
RA Kapral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Greenkin G., Zhu L.,

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RA Vasteva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fontein M., Kyryides N.C., Overbeek R.,
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT nucleatum strain ATCC 25586.";
 RL J. Bacteriol. 184:2005-2018(2002).
 CC -1 - SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AE010577; MAL94856.1; -.
 DR HSSP; Q58206; 1L2T.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 KM SEQUENCE 335 AA; 37442 MW; E6ABF4100E7B4C3B CRC64;
 SQ
 Query Match 83.8%; Score 31; DB 2; Length 335;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSNLHS 7
 DB 11 YSNNLHA 17
 RESULT 39
 Q9L906 PRELIMINARY; PRT; 347 AA.
 ID Q9L906;
 AC Q9L906;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glycoyltransferase (Putative Beta-1,4-N-
 DE acetylglucosaminyltransferase).
 GN Name=cgta;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OC NCBI_TaxId=197;
 RX MEDLINE=20127662; PubMed=10660542;
 RX STRAIN=ATCC 43446;
 RA Cummingham A.M., Wu Y., Young N.M., Wakarchuk W.W.,
 RA Gilbert M., Brisson J.R., Karwaski M.F., Michniewicz J.,
 RT "Biosynthesis of ganglioside mimics in Campylobacter jejuni OH4394.
 RT Identification of the glycoyltransferase genes, enzymatic synthesis
 RT of model compounds, and characterization of nanomole amounts by 600-
 RT mhz (1)h and (13)C NMR analysis.";
 RL J. Biol. Chem. 275:3896-3906(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43446;
 RA Gilbert M.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB11;
 RX PubMed=14742567;
 RX Gilbert M., Godschalk P.C., Karwaski M.F., Ang C.W., Van Belkum A.,
 RA Li J., Wakarchuk W.W., Endtz H.P.;
 RT "Evidence for Acquisition of the Lipooligosaccharide Biosynthesis
 RT locus in Campylobacter jejuni GB11, a Strain Isolated from a Patient
 RT with Guillain-Barre Syndrome, by Horizontal Exchange.";
 RL Infect. Immun. 72:1162-1165(2004).

DR EMBL; AF167344; AAF34142.1; -.
 DR EMBL; AY422197; AAR82873.1; -.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR InterPro; IPR010446; Cgta.
 DR Pfam; PF06306; Cgta; 1.
 KW Transferase
 SQ SEQUENCE 347 AA; 41818 MW; 24006D7C9C180C4 CRC64;
 SQ
 Query Match 83.8%; Score 31; DB 2; Length 347;
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSNLHS 7
 DB 268 FSSNLHS 274
 RESULT 40
 Q9LAK4 PRELIMINARY; PRT; 347 AA.
 ID Q9LAK4;
 AC Q9LAK4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-1,4-N-acetylglucosaminyltransferase.
 DE Name=cgta;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OC NCBI_TaxId=197;
 RX MEDLINE=20127662; PubMed=10660542;
 RX STRAIN=OH4384;
 RA Cummingham A.M., Wu Y., Young N.M., Wakarchuk W.W.,
 RA Gilbert M., Brisson J.R., Karwaski M.F., Michniewicz J.,
 RT "Biosynthesis of ganglioside mimics in Campylobacter jejuni OH4394.
 RT Identification of the glycoyltransferase genes, enzymatic synthesis
 RT of model compounds, and characterization of nanomole amounts by 600-
 RT mhz (1)h and (13)C NMR analysis.";
 RL J. Biol. Chem. 275:3896-3906(2000).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OH4384;
 RA Gilbert M.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43446;
 RA Gilbert M.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB11;
 RX PubMed=14742567;
 RX Gilbert M., Godschalk P.C., Karwaski M.F., Ang C.W., Van Belkum A.,
 RA Li J., Wakarchuk W.W., Endtz H.P.;
 RT "Evidence for Acquisition of the Lipooligosaccharide Biosynthesis
 RT locus in Campylobacter jejuni GB11, a Strain Isolated from a Patient
 RT with Guillain-Barre Syndrome, by Horizontal Exchange.";
 RL Infect. Immun. 72:1162-1165(2004).

Search completed: December 17, 2004, 19:14:42
 Job time : 22.9213 secs

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OM protein - protein search, using sw model

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118.029 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQYSKLPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

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Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

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Database :

1: A_Geneseq_23Sep04:*
2: geneseqp1908:*
3: geneseqp1908:*
4: geneseqp2000:*
5: geneseqp2000:*
6: geneseqp2003:*
7: geneseqp2003:*
8: geneseqp2004:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	9	4	AAB81984	Aab81984 Gangliosid
2	56	100.0	9	6	ABU11009	Abu11009 Modified
3	56	100.0	108	4	AAB81988	Aab81988 Gangliosid
4	56	100.0	108	4	AAB81986	Aab81986 Gangliosid
5	56	100.0	108	4	AAB81990	Aab81990 Gangliosid
6	56	100.0	108	6	ABU11011	Abu11011 Modified
7	56	100.0	108	6	ABU11013	Abu11013 Modified
8	56	100.0	128	2	AAR33257	Rat Immun
9	56	100.0	128	2	AAR53340	K6641 H c
10	56	100.0	128	2	AAV28368	pkM641 LA
11	56	100.0	128	3	AAB01628	Murine im
12	56	100.0	128	4	AAB81994	Aab81994 Gangliosid
13	56	100.0	128	4	AAB81995	Aab81995 Gangliosid
14	56	100.0	128	4	AAB81997	Aab81997 Gangliosid
15	56	100.0	128	4	AAB81978	Aab81978 Gangliosid
16	56	100.0	128	4	AAB81996	Aab81996 Gangliosid
17	56	100.0	128	4	AAB81999	Aab81999 Gangliosid
18	56	100.0	128	4	AAB81993	Aab81993 Gangliosid
19	56	100.0	128	4	AAB81992	Aab81992 Gangliosid
20	56	100.0	128	6	ABU11003	Abu11003 Modified
21	56	100.0	126	2	AAR12237	Mouse Mab
22	48	85.7	127	2	AAR12359	Light (ka
23	44	78.6	109	6	ADA89188	Human ant
24	43	76.8	215	5	ABP43158	Human ova

26	42	75.0	107	8	AD007305	Ado07305 Human pro
27	42	75.0	107	8	AD007307	Ado07307 Human pro
28	41	73.2	113	4	AAB48936	Aab48936 Anti-TrkA
29	41	73.2	295	4	AAB48934	Aab48934 Anti-TrkA
30	40	71.4	9	3	AAB06354	Aab06354 Randomise
31	40	71.4	9	3	AAB06352	Aab06352 Randomise
32	40	71.4	107	2	AAR30770	Aar30770 Consensus
33	40	71.4	107	4	AAB62087	Aab62087 Human VI
34	40	71.4	107	4	AAB60400	Aab60400 Consensus
35	40	71.4	107	4	AAB61585	Aab61585 Human var
36	40	71.4	107	8	AD071454	Ad071454 Human ant
37	40	71.4	107	8	AD086008	Ad086008 Human var
38	40	71.4	107	8	ADN12054	Adn12054 Variable
39	40	71.4	107	8	ADP43328	Adp43328 Human mon
40	40	71.4	108	2	AAW04177	Aw04177 Variant v
41	40	71.4	108	2	AAW00834	Aw00834 Variable
42	40	71.4	108	2	AAW16620	Aw16620 Anti-huma
43	40	71.4	108	2	AAW70622	Aw70622 Human con
44	40	71.4	108	3	AAW82345	Aw82345 Human con
45	40	71.4	108	4	AAE12062	Aae12062 Human ant

ALIGNMENTS

RESULT 1	
AAB81984	
ID	AAB81984 standard; peptide; 9 AA.
XX	
AC	AAB81984;
DT	03-JUL-2001 (first entry)
XX	
DE	Ganglioside GD3 specific antibody related peptide SEQ ID NO: 8.
XX	
KW	Ganglioside; GD3; complementarity determining region; CDR; antibody;
KM	Cancer.
XX	
OS	Mus musculus.
XX	
PN	WO200123432-A1.
PD	
XX	
PF	29-SEP-2000; 2000WO-JP006774.
XX	
PR	30-SEP-1999; 99JP-00278291.
XX	
PR	06-APR-2000; 2000JP-00105088.
XX	
PA	(KYOW) KYOWA HAKKO KOGYO KK.
XX	
PI	Hanai N, Shitara K, Nakamura K, Niwa R;
XX	
DR	WPI; 2001-266143/27.
XX	
PT	New human type complementation-determining region-transplanted antibody
PT	and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT	of e.g. tumors, with low antigenicity, little side effects but potent
PT	activity in cancer.
XX	
PS	Claim 4; Page 142; 183pp; Japanese.
XX	
CC	The present invention describes a monoclonal antibody which can react
CC	specifically with ganglioside GD3. The antibody and its derivatives are
CC	useful in the diagnosis and therapy of tumors, particularly cancer
CC	diagnosis. The present sequence is a protein used in the exemplification
CC	of the invention
XX	
SO	Sequence 9 AA;
Query Match	100.0%; Score 56; DB 4; Length 9;
Best Local Similarity	100.0%; Pred. No. 1.7e+06;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 HQYSKLPWT 9
      |||||
      1 HQYSKLPWT 9

Db

RESULT 2
ABU11009
ID      ABU11009 standard; peptide; 9 AA.
XX
XX
AC      ABU11009;
XX
DT      04-FEB-2003 (first entry)
XX
DE      Modified ganglioside GD3 antibody associated peptide #6.
XX
XX      Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS      Mus musculus.
XX
PN      W0200278739-A1.
XX
PD      10-OCT-2002.
XX
PF      29-MAR-2002; 2002WO-JP003170.
XX
PR      29-MAR-2001; 2001JP-00097483.
XX
PA      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI      Shitara K, Niwa R, Kanazawa J, Asada M;
XX
DR      WPI; 2003-067410/06.
XX
PT      Drugs containing genetically-modified antibody against ganglioside GD3,
PT      its fragment, immunocompetent cell activators or/and antitumor agents in
PT      combination, applicable in treating malignant tumor like melanoma.
XX
XX
PS      Claim 6; Page 99; 121pp; Japanese.
XX
CC      The invention describes drugs contain a genetically-modified antibody
CC      against ganglioside GD3 or its fragment and at least 1 of a substance
CC      capable of activating immunocompetent cells and a substance having an
CC      antitumor activity in combination. The drugs can be used to treat tumour
CC      like melanoma and can provide a treatment with enhanced therapeutic
CC      effect and little side-reactions, particularly to relieve problems of
CC      side-effects during the conventional single administration. This sequence
CC      represents a peptide associated with the anti- ganglioside GD3 antibody
CC
SQ      Sequence 9 AA;

Query Match      100.0%; Score 56; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 HQYSKLPWT 9
      |||||
      1 HQYSKLPWT 9

Db

RESULT 3
AAB81988
ID      AAB81988 standard; protein; 108 AA.
XX
XX
AC      AAB81988;
XX
DT      03-JUL-2001 (first entry)
XX
DE      Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
XX
XX      Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX      cancer.
XX

```

```

OS      Synthetic.
XX
XX      W0200123432-A1.
XX
XX
PD      05-APR-2001.
XX
XX      29-SEP-2000; 2000WO-JP006774.
XX
XX      30-SEP-1999; 99JP-00278291.
XX
PR      06-APR-2000; 2000JP-00105088.
XX
XX      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PA      Hanai N, Shitara K, Nakamura K, Niwa R;
XX
PI      WPI; 2001-266143/27.
XX
DR      New human type complementation-determining region-transplanted antibody
PT      and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT      of e.g. tumors, with low antigenicity, little side effects but potent
PT      activity in cancer.
XX
XX
PS      Claim 22; Page 172-173; 183pp; Japanese.
XX
XX
CC      The present invention describes a monoclonal antibody which can react
CC      specifically with ganglioside GD3. The antibody and its derivatives are
CC      useful in the diagnosis and therapy of tumours, particularly cancer
CC      diagnosis. The present sequence is a protein used in the exemplification
CC      of the invention
CC
SQ      Sequence 108 AA;

Query Match      100.0%; Score 56; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 HQYSKLPWT 9
      |||||
      89 HQYSKLPWT 97

Db

RESULT 4
AAB81986
ID      AAB81986 standard; protein; 108 AA.
XX
XX
AC      AAB81986;
XX
DT      03-JUL-2001 (first entry)
XX
XX
DE      Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
XX
XX      Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX      cancer.
XX
OS      Synthetic.
XX
PN      W0200123432-A1.
XX
PD      05-APR-2001.
XX
XX      29-SEP-2000; 2000WO-JP006774.
XX
XX      30-SEP-1999; 99JP-00278291.
XX
PR      06-APR-2000; 2000JP-00105088.
XX
XX      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PA      Hanai N, Shitara K, Nakamura K, Niwa R;
XX
PI      WPI; 2001-266143/27.
XX
DR      New human type complementation-determining region-transplanted antibody
PT      and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT

```

PT of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

XX Example 1, Page 143-144; 183pp; Japanese.

PS The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
DB 89 HOYSKLPMT 97

RESULT 5

AB81990
ID AAB81990 standard; protein; 108 AA.

XX AAB81990;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX Mus musculus.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000MO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

XX 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

XX Claim 11, Page 174-175; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
DB 89 HOYSKLPMT 97

DB 89 HOYSKLPMT 97

RESULT 6

ABU1011
ID ABU1011 standard; protein; 108 AA.

XX ABU1011;

XX 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated protein #4.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Synthetic.

XX WO200278739-A1.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002MO-JP003170.

XX 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drug containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and anticancer agents in
PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 8, Page 100; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
DB 89 HOYSKLPMT 97

RESULT 7

ABU1013
ID ABU1013 standard; protein; 108 AA.

XX ABU1013;

XX 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated protein #6.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.

XX WO200278739-A1.

XX

PD 10-OCT-2002. XX
XX
PF 29-MAR-2002; 2002WO-JP003170. XX
XX
PR 29-MAR-2001; 2001JP-00097483. XX
XX
PA (KYOW) KYOWA HAKKO KOGYO KK. XX
XX
P1 Shitara K, Niwa R, Kanazawa J, Asada M, XX
XX
DR WPI; 2003-067410/06. XX
XX
PT Drugs containing genetically-modified antibody against ganglioside GD3, XX
PT its fragment, immunocompetent cell activators or/and antitumor agents in XX
PT combination, applicable in treating malignant tumor like melanoma. XX
PS
PS Claim 7; Page 113; 121pp; Japanese. XX
XX
XX The invention describes drugs contain a genetically-modified antibody XX
CC against ganglioside GD3 or its fragment and at least 1 of a substance XX
CC capable of activating immunocompetent cells and a substance having an XX
CC antitumor activity in combination. The drugs can be used to treat tumour XX
CC like melanoma and can provide a treatment with enhanced therapeutic XX
CC effect and little side-reactions, particularly to relieve problems of XX
CC side-effects during the conventional single administration. This sequence XX
CC represents a protein associated with the anti- ganglioside GD3 antibody XX
XX
XX Sequence 108 AA; XX
XX

```
Query Match      100.0%   Score 56:  DB 6:   length 108;
Best Local Similarity 100.0%   Pred. NC 0.043;
Matches      9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

QY	1	HQYSKLPWT	9
Db	89	HQYSKLPWT	97

RESULT 8
AAR33257
ID AAR33257 standard; protein; 128 AA.
...

DT	25-MAR-2003	(revised)
DT	12-JUL-1993	(first entry)

DE Rat immunoglobulin L chain variable region of pKM641LA2.

KM Promoter; variable; region; rat; immunoglobulin; heavy; H; chain.
KM humanised: chimeric; antibody; expression vector.

OS Rattus rattus.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT	Protein	/note= "Signal peptide"
FT		21. .128

PN EP533199-A2

PD 24-MAR-1993

PF 18-SEP-1992; 92EP-00116026.

PR 18-SEP-1991; 91JP-00238375.

PA (KYOW) KYOWA HAKKO KOGYO CO LTD.

PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y,

DR WPI; 1993-095510/12.

DR N-PSDB; AAQ33258.

PT Humanised chimeric antibody prodn. aganst ganglioside GD3 - for treating
PT cancers, such as melanoma, neuroblastoma, etc.

PS Claim 6; Page 30-31; 63pp; English.

CC The sequences given in AAR3325c-57 represent rat heavy and light chain
CC variable regions respectively. The DNA sequences encoding these proteins
CC were used in the construction of humanised chimeric antibody expression
CC vectors. In these humanised antibodies none of the amino acids of the non
CC -human animal Ab variable region have been changed. (Updated on 25-MAR-
CC 2003 to correct PN field.)

SQ Sequence 128 AA;

Query Match	100.0%	Score 56;	DB 2;	length 128;
Similarity	100.0%	Pred. No. 0.051;		
Best Local	9;	Conservative	0;	Indels 0;
Matches	9;	Conservative	0;	Gaps 0;

QY 1 HQYSLPWT 9
|||
Db 109 HQYSLPWT 117

RESULT 9
AAR53340
ID AAR53340 standard; protein; 128 AA

DT	18-NOV-1994	(first entry)
XX		
DE	KM641 H chain variable region	

KM Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody
KM expression vector; heavy, light, hypervariable region; CDR
KM constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.

OS Mus musculus

Key	Location/Qualifiers
EH	1. .20
FT	/label= sig_peptide
FT	

PN AU9346181-A.

PD 17-MAR-1994

PF 07-SEP-1993; 93AU-00046181.

PR 07-SEP-1992; 92JP-00238452.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;

DR WPI; 1994-126857/16.

XXIX

cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.

PS Example 2; Page 115-116; 191pp; English.

CC Example describes the construction of the vector pCk1641HA1 for
CC chimeric human antibody H chain expression. mRNA from mouse anti-GP3
CC monoclonal Ab K6641-producing cells was isolated and K6641 H and L chain
CC cDNAs isolated. The base sequences of the Ig variable regions in K6641 H
CC chain cDNA (pK6641HA3) and K6641 L chain cDNA (pK6641LA2) are given in
CC AAG45438-39. A K6641-derived chimeric human Ab H chain expression vector
CC was constructed by joining the H chain variable region gene from
CC pK6641HA3 to a vector for chimeric human Ab H chain expression using the

CC synthetic DNAs given in AAG63439 and AAG63440
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

RESULT 10
AAY28368
ID AAY28368 standard; protein; 128 AA.

XX AAY28368;

DT 04-NOV-1999 (first entry)

DE PKM641 IAA2 immunoglobulin light chain.

XX antibody; nucleotide; genomic; hypervariable region; chimeric;

KM light chain; amino acid.

XX Mus sp.

OS US5939532-A.

PN 17-AUG-1999.

XX 07-JUN-1995; 95US-00483528.

XX 07-SEP-1993; 93US-00116778.

PR (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;

XX WPI; 1999-468416/39.

DR N-PSDB; AAA93481.

XX Chimeric human antibody expression vectors.

XX Example 1; Col 99; 188pp; English.

XX This immunoglobulin region was isolated from PKM641IAA2.A methionine
CC codon, presumably the initiation codon ATG, was found in the vicinity of
CC the 5' terminus and the sequence has a full length leader sequence. The
CC chimeric human antibodies are useful in the treatment of cancer,
CC especially that which is of neural ectodermal origin. In contrast to
CC prior art constructs based on mouse monoclonal antibodies, the chimeric
CC human antibodies do not cause anti-mouse immunoglobulin production. The
CC chimeric human antibodies have a prolonged half-life and a reduced
CC frequency of adverse effects when compared to mouse monoclonal antibodies
SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

RESULT 11
AAB01628
ID AAB01628 standard; protein; 128 AA.
XX
AC AAB01628;

XX 07-DEC-2000 (first entry)

DE Murine immunoglobulin light chain variable region.

XX Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
XX humanised antibody.

XX Mus sp.

PH Key Location/Qualifiers

FT Peptide 1..20 /label= signal_peptide

FT Protein 21..128 /label= mature_immunoglobulin_light_chain_V_region

XX EP1013761-A2.

XX 28-JUN-2000.

XX 18-SEP-1992; 99EP-00124345.

XX 18-SEP-1991; 91JP-00238375.

XX 18-SEP-1992; 92EP-00116026.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

XX WPI; 2000-402204/35.

XX N-PSDB; AAA51004.

XX New humanized chimera antibody KM-871 useful for treating cancer,
PT comprises variable region of mouse monoclonal antibody, reactive with
PT ganglioside and human antibody constant region.

XX Claim 14; Page 28-29; 65pp; English.

XX The present sequence is a murine immunoglobulin light chain variable
CC region from plasmid KM-641. The coding sequence was used in the creation
CC of an expression vector, along with the sequence for a human antibody, to
CC produce humanised chimaeric antibodies, which can be used to treat
CC cancer. Humanised chimaeric antibodies are more effective than mouse
CC antibodies as they do not provoke a reaction in the human and side
CC effects, such as the formation of anti-mouse immunoglobulin antibody and
CC the rapid half-life of the immunoglobulins, do not occur
XX

SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

RESULT 12
AAB81994
ID AAB81994 standard; protein; 128 AA.

XX AAB81994;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #3.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX Synthetic.

```

PN      WO200123432-A1.
XX
PD      05-APR-2001.
XX
PF      29-SEP-2000; 2000WO-JP006774.
XX
PR      30-SEP-1999; 99JP-00278291.
XX      06-APR-2000; 2000JP-00105088.
XX
PA      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI      Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR      WPI; 2001-266143/27.
XX      N-PSDB; AAF86898.
XX
PT      New human type complementation-determining region-transplanted antibody
PT      and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT      of e.g. tumors, with low antigenicity, little side effects but potent
PT      activity in cancer.
XX
PS      Example 1; Page 155-156; 183pd; Japanese.
XX
CC      The present invention describes a monoclonal antibody which can react
CC      specifically with ganglioside GD3. The antibody and its derivatives are
CC      useful in the diagnosis and therapy of tumors, particularly cancer
CC      diagnosis. The present sequence is a protein used in the exemplification
CC      of the invention
XX
SQ      Sequence 128 AA;
XX
Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HOYSKLPWT 9
        |||||||
Db       109 HOYSKLPWT 117

RESULT 13
AAB81995
ID      AAB81995 standard; protein; 128 AA.
XX
AC      AAB81995;
XX
DT      03-JUL-2001 (first entry)
XX
DE      Ganglioside GD3 specific antibody related protein #4.
XX
KW      Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW      cancer.
XX
OS      Synthetic.
XX
PN      WO200123432-A1.
XX
PD      05-APR-2001.
XX
PF      29-SEP-2000; 2000WO-JP006774.
XX
PR      30-SEP-1999; 99JP-00278291.
XX      06-APR-2000; 2000JP-00105088.
XX
PA      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI      Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR      WPI; 2001-266143/27.
XX      N-PSDB; AAF86901.
XX
PT      New human type complementation-determining region-transplanted antibody
PT      and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT      of e.g. tumors, with low antigenicity, little side effects but potent
PT      activity in cancer.
XX
PS      Example 1; Page 155-156; 183pd; Japanese.
XX
CC      The present invention describes a monoclonal antibody which can react
CC      specifically with ganglioside GD3. The antibody and its derivatives are
CC      useful in the diagnosis and therapy of tumors, particularly cancer
CC      diagnosis. The present sequence is a protein used in the exemplification
CC      of the invention
XX
SQ      Sequence 128 AA;
XX
Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HOYSKLPWT 9
        |||||||
Db       109 HOYSKLPWT 117

```

```

PT of e.g.tumors, with low antigenicity, little side effects but potent
PR activity in cancer.
XX
XX Example 1; Page 157-158; 183pp; Japanese.
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPMT 9
        |||||
Db       109 HOYSKLPMT 117

RESULT 14
AAB81997 standard; protein; 128 AA.
ID AAB81997
XX
XX AAB81997;
AC
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein #6.
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
XX Synthetic.
OS
XX WO200123432-A1.
PN
XX PD 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX PA (KYOW ) KYOMA HAKKO KOGYO KK.
XX
XX PI Hamai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX DR N-PSDB; AAF66907.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 161-162; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPMT 9

```

Db |||||
109 HQYSKLPWT 117

RESULT 15

AAAB81978 standard; protein; 128 AA.

AC AAB81978;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Mus musculus.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI: 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

PS Example 1; Page 140; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumors, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

CC of the invention

Query Match 100.0%; Score 56; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 0.051; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9

DB 109 HQYSKLPWT 117

RESULT 16

AAAB81996 standard; protein; 128 AA.

AC AAB81996;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #5.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI: 2001-266143/27.

DR N-PSDB; AAF86904.

PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

PS Example 1; Page 159-160; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumors, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

CC of the invention

Query Match 100.0%; Score 56; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 0.051; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9

DB 109 HQYSKLPWT 117

RESULT 17

AAAB81999 standard; protein; 128 AA.

AC AAB81999;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #8.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI: 2001-266143/27.

DR N-PSDB; AAF86913.

PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
PS Example 1; Page 166; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117
RESULT 18
AAB81993
ID AAB81993 standard; protein; 128 AA.
XX
AC AAB81993;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #2.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
DR N-PSDB; AAF86895.
XX
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 153; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

DB 109 HOYSKLPWT 117
RESULT 19
AAB81992
ID AAB81992 standard; protein; 128 AA.
XX
AC AAB81992;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #1.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
DR N-PSDB; AAF86892.
XX
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 150-151; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117
RESULT 20
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
AC AAB81998;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #7.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
OS Synthetic.

XX WO200123432-A1.
 PN 05-APR-2001.
 XX
 XX 29-SEP-2000; 2000WO-JP006774.
 PF
 XX 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 PI WPI; 2001-266143/27.
 DR N-PSDB; AAF86912.
 DR
 XX New human type complementation-determining region-transplanted antibody
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 PS Example 3; Page 164-165; 183pp; Japanese.
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 XX
 SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 4; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
 DB 109 HOYSKLPWT 117

RESULT 21
 ABU11003
 ID ABU11003 standard; protein; 128 AA.
 XX
 XX ABU11003;
 AC
 XX 04-FEB-2003 (first entry)
 DT
 XX Modified ganglioside GD3 antibody associated protein #2.
 DE
 XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 KM
 XX Mus musculus.
 OS
 XX WO200278739-A1.
 PN
 XX 10-OCT-2002.
 PD
 XX 29-MAR-2002; 2002WO-JP003170.
 PF
 XX 29-MAR-2001; 2001JP-00097483.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Shitara K, Niwa R, Kanazawa J, Asada M;
 PI WPI; 2003-067410/06.
 DR
 XX Drug containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX

PS Example 3; Page 98; 121pp; Japanese.
 CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 XX
 SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 6; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
 DB 109 HOYSKLPWT 117

RESULT 22
 AAR12237
 ID AAR12237 standard; protein; 126 AA.
 XX
 XX AAR12237;
 AC
 XX 25-MAR-2003 (revised)
 DT 19-AUG-1991 (first entry)
 DT
 XX Mouse Mab 1C11 L chain V region.
 DE
 XX HIV-1; chimera.
 KM
 XX Mus sp.
 OS
 XX WO9107494-A.
 PN
 XX 30-MAY-1991.
 PD
 XX 13-NOV-1989; 89US-00433703.
 PF
 XX 13-NOV-1989; 89US-00433703.
 PR
 XX (XOMA) XOMA CORP.
 PA (GREG) GREEN CROSS CORP.
 PA (ZOMA-) ZOMA CORP.
 XX
 XX Better MD, Horwitz AH, Ghoshdastgi P, Robinson RR;
 PI WPI; 1991-178106/24.
 DR N-PSDB; AAQ12017.
 DR
 XX New chimeric mouse human antibodies - used in treatment, diagnosis and
 PT prophylaxis of HIV infections.
 PT
 XX Disclosure; Fig 13; 108pp; English.
 PS
 XX The mouse VL gene product may be used to produce chimeric mouse- human
 CC Abs against HIV-1 comprising human Ig constant regions and murine
 CC variable regions. These novel sequence are useful in treatment, diagnosis
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 CC
 XX
 SQ Sequence 126 AA;

Query Match 85.7%; Score 48; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYSKLPWT 9

Db 110 QYSKLPWT 117
RESULT 23
AAR12359
ID AAR12359 standard; protein; 127 AA.
XX
XX AAR12359;
AC
XX
XX 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
XX
XX Light (kappa) chain variable region of murine IC11 immunoglobulin.
DE
XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
XX Mus musculus.
OS
XX WO9107493-A.
PN 30-MAY-1991.
PD
XX 13-NOV-1989; 89US-00433730.
XX
XX 13-NOV-1989; 89US-00433730.
PR
XX 13-NOV-1989; 89US-00433730.
XX
XX (XOMA) XOMA CORP.
PA (GREG) GREEN CROSS CORP.
XX
XX PI Better MD, Horwitz AH, Ghoshdastgi P, Robinson R;
XX
XX MPI; 1991-178105/24.
DR N-PSDB; AAQ12061.
XX
XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
XX
XX Disclosure; Fig 13; 107pp; English.
XX
XX This is the light (kappa) - chain variable (V) region of a mouse
CC monoclonal antibody (MAb), 1C11, and is specific for an HIV-1 viral
CC antigen. It is used in the construction of a chimeric MAb comprising
CC heavy and light chains having murine V regions and human C regions. The
CC chimeric MAbs are more effective than murine MAb 1C11 since they have an
CC increased compatibility in humans. The heavy and light chain V-regions
CC are joined by manipulating their respective joining (J) regions, to
CC generate restriction enzyme recognition sites. The chimeric MAbs can be
CC used as immunoconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
CC 60 and AAQ12062-63. (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to
CC correct DR field.)
XX
XX Sequence 127 AA;
SQ
Query Match 85.7%; Score 48; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QYSKLPWT 9
Db 110 QYSKLPWT 117
RESULT 24
ADA89188
ID ADA89188 standard; protein; 109 AA.
XX
XX ADA89188;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX

DE Human antibody 2B2 light chain amino acid sequence SEQ ID NO:32.
XX
XX Immunoglobulin; Ig; heavy chain variable domain;
XX light chain variable domain; major histocompatibility complex; MHC;
XX gp100; MUC1; TAX; hTERT; cytosolic; gene therapy; cancerous disorder;
XX cancer.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO2003070752-A2.
PN 28-AUG-2003.
PD
XX 20-FEB-2003; 2003WO-US005128.
XX
XX 20-FEB-2002; 2002US-0358994P.
PR
XX (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX Hoogenboom HRJM, Reiter Y;
XX
XX MPI; 2003-663847/62.
DR N-PSDB; ADA89187.
XX
XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX
XX Disclosure; Fig 7A; 224pp; English.
XX
XX The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC NUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytosolic activity,
CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the light chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
XX gp100.
XX
XX Sequence 109 AA;
SQ
Query Match 78.6%; Score 44; DB 6; Length 109;
Best Local Similarity 77.8%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
Db 90 HOYGFLPWT 98
RESULT 25
ABP43158
ID ABP43158 standard; protein; 215 AA.

XX ABP43158;
 AC 22-AUG-2002 (first entry)
 DT
 XX Human ovarian antigen HVC185, SEQ ID NO:4290.
 DE
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
 XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 XX inflammatory condition; immune disorder; blood disorder;
 XX cardiovascular disorder; respiratory disorder; neurological disorder;
 XX gastrointestinal disorder; urinary system disorder; drug screening;
 XX gene therapy; chromosome mapping; forensic analysis;
 XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 XX antiinflammatory; gynaecological; reproductive.
 OS Homo sapiens.
 XX WO200200677-A1.
 PN 03-JAN-2002.
 XX 07-JUN-2001; 2001WO-US018569.
 XX 07-JUN-2000; 2000US-0209467P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX Birse CE, Rosen CA;
 PI WPI: 2002-147878/19.
 DR N-PSDB; ABO56235.
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX Claim 11; SEQ ID NO 4290; 2922bp; English.
 PS
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABO54131-ABO56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptide may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence in represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 215 AA;

Query Match 76.8%; Score 43; DB 5; Length 215;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YSKLPWT 9
 DB 196 YSKLPWT 202
 RESULT 26
 ADO07305
 ID ADO07305 standard; protein; 107 AA.
 AC ADO07305;
 XX 15-JUL-2004 (first entry)
 DT
 XX Human proteolytic A26-JNK1 light chain, used in catalytic antibody.
 XX Catalytic antibody; human; antibody; protease; gene therapy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1..23
 FT Region /label= FR1
 FT /note= "Framework region 1"
 FT Active-site
 FT 1
 FT /note= "Possible Glu component of catalytic triad"
 FT 24..34
 FT Region /label= CDR1
 FT /note= "Complementarily determining region 1"
 FT 25
 FT /note= "Possible Ser component of catalytic triad"
 FT 28
 FT /note= "Possible Ser component of catalytic triad"
 FT 31
 FT /note= "Possible Ser component of catalytic triad"
 FT 32
 FT /note= "Possible Ser component of catalytic triad"
 FT 34
 FT /note= "Possible His component of catalytic triad"
 FT Region 35..49
 FT /label= FR2
 FT /note= "Framework region 2"
 FT 50..56
 FT Region /label= CDR2
 FT /note= "Complementarily determining region 2"
 FT 52
 FT /note= "Possible Ser component of catalytic triad"
 FT 54
 FT /note= "Possible Ser component of catalytic triad"
 FT 56
 FT /note= "Possible Ser component of catalytic triad"
 FT 57..88
 FT Region /label= FR3
 FT /note= "Framework region 3"
 FT 89..95
 FT Region /label= CDR3
 FT /note= "Complementarily determining region 3"
 FT 89
 FT /note= "Possible His component of catalytic triad"
 FT 91
 FT /note= "Possible Ser component of catalytic triad"
 FT 92
 FT /note= "Possible Ser component of catalytic triad"
 FT 93
 FT /note= "Possible Ser component of catalytic triad"
 FT 93
 FT /note= "Possible Ser component of catalytic triad"
 XX MO2004033658-A2.
 XX 22-APR-2004.
 PD

CC comprise a human antibody light chain operably joined to a heterologous
CC antibody heavy chain. The light chain has a serine protease dyad and
CC endopeptidase activity, and the heavy chain has a predetermined
CC specificity for a target protein. By joining 2 heterologous human
CC antibody chains, one of which supplies the catalytic activity to
CC hydrolyse polypeptides and the other the binding specificity for a target
CC protein, the invention provides for the construction of a repertoire of
CC processes with customised protein substrate specificities of potentially
CC unlimited number and thus makes possible the effective treatment and/or
CC prevention of any medical condition attributable to the presence or
CC overexpression of an identified protein. The invention also provides
CC nucleic acids encoding the catalytic antibodies (which can be used for
CC gene therapy), host cells, transgenic non-human animals, and methods of
CC cleaving a target protein (in vitro or in vivo) using a recombinant
CC catalytic polypeptide. It also provides a library of recombinant
CC catalytic polypeptides with altered enzymatic activity, and a method of
CC altering the enzymatic activity of the recombinant catalytic polypeptides
CC by mutating at least one complementarily determining region of the heavy
CC chain.

SQ Sequence 107 AA;

Query Match 75.0%; Score 42; DB 8; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 HOYSKLPWT 9
||| |||
Db 89 HQSSSLPWT 97

RESULT 28
AAB48936
ID AAB48936 standard; protein; 113 AA.

AC AAB48936;

DT 16-MAR-2001 (first entry)

DE Anti-TrkA murine monoclonal antibody MNAC13 light chain variable region.

KW Murine monoclonal antibody MNAC13; light chain variable region; VL;

KW human TrkA antagonist; NGF receptor; nerve growth factor;

KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;

KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging; diagnosis.

OS Mus sp.

PN WO20007344-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000MO-IT000218.

XX 26-MAY-1999; 99IT-RM000333.

XX (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.

XX Novak MM;

XX MPI; 2001-061515/07.

XX N-PSDB; AAC87642.

XX Monoclonal antibody and its derivatives specific to high affinity

XX tyrosine kinase receptor of nerve growth factor useful for treating and

XX diagnosing neuropathological disorders such as pain, neuromas, TrkA

XX expressing neoplastic tumors.

XX Claim 2; Page; 33pp; English.

XX The invention relates to a murine monoclonal antibody, MNAC13, which

XX recognises the human nerve growth factor (NGF) receptor tyrosine kinase,

XX TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13 has a light

CC chain variable region (VL) as given in AAB48936, and a heavy chain
CC variable region (VH) as given in AAB48937. The invention also encompasses
CC synthetic derivatives of monoclonal antibody MNAC13, such as the single
CC chain antibody, scFvMNAC13 (AAB48934), which comprises the VL and VH
CC regions of MNAC13 in one polypeptide chain. The invention additionally
CC relates to pharmaceutical compositions comprising the antibody or
CC antibody derivatives of the invention, engineered eukaryotic cells able
CC to express the MNAC13 antibody or its derivatives, and a diagnostic
CC composition comprising the antibody or its derivatives for in vivo
CC imaging. NGF antagonist (inhibitor of binding of NGF to TrkA receptor The
CC MNAC13 monoclonal antibody and its derivatives are useful for treating
CC neurological pathologies such as acute or chronic pain, neuromas, and
CC TrkA-expressing neoplastic tumors. A composition comprising MNAC13 or
CC its derivatives with a diagnostically acceptable carrier is useful for in
CC vivo imaging diagnostics. The present sequence represents the light chain
CC variable region of the anti-TrkA murine monoclonal antibody MNAC13. Note:
CC The present sequence is derived from that of the single chain antibody
CC scFvMNAC13 shown on pages 32-33 and the information given in claim 2
CC

SQ Sequence 113 AA;

Query Match 73.2%; Score 41; DB 4; Length 113;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 HOYSKLPWT 9
||| |||
Db 89 HQSSSLPWT 97

RESULT 29
AAB48934
ID AAB48934 standard; protein; 295 AA.

AC AAB48934;

DT 16-MAR-2001 (first entry)

DE Anti-TrkA single chain antibody scFvMNAC13.

KW Single chain antibody; murine monoclonal antibody MNAC13; scFvMNAC13;

KW human TrkA antagonist; NGF receptor; nerve growth factor;

KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;

KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging; diagnosis.

OS Mus sp.

PN WO20007344-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000MO-IT000218.

XX 26-MAY-1999; 99IT-RM000333.

XX (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.

XX Novak MM;

XX MPI; 2001-061515/07.

XX N-PSDB; AAC87642.

XX Monoclonal antibody and its derivatives specific to high affinity

XX tyrosine kinase receptor of nerve growth factor useful for treating and

XX diagnosing neuropathological disorders such as pain, neuromas, TrkA

XX expressing neoplastic tumors.

XX Claim 8; Page 32-33; 33pp; English.

XX The invention relates to a murine monoclonal antibody, MNAC13, which

XX recognises the human nerve growth factor (NGF) receptor tyrosine kinase,

XX TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13 has a light

CC chain variable region (VL) as given in AAB48936, and a heavy chain
CC variable region (VH) as given in AAB48937. The invention also encompasses
CC synthetic derivatives of monoclonal antibody MNAC13, such as the single
CC chain antibody, scFvMNAC13 (AAB48934), which comprises the VL and VH
CC regions of MNAC13 in one polypeptide chain. The invention additionally
CC relates to pharmaceutical compositions comprising the antibody or
CC antibody derivatives of the invention, engineered eukaryotic cells able
CC to express the MNAC13 antibody or its derivatives, and a diagnostic
CC composition comprising the antibody or its derivatives for in vivo
CC imaging. NGF antagonist (inhibitor of binding of NGF to TrkA receptor. The
CC MNAC13 monoclonal antibody and its derivatives are useful for treating
CC neurological pathologies such as acute or chronic pain, neuromas, and
CC TrkA-expressing neoplastic tumours. A composition comprising MNAC13 or
CC its derivatives with a diagnostically acceptable carrier is useful for in
CC vivo imaging diagnostics. The present sequence represents the anti-TrkA
CC single chain antibody scFvMNAC13
XX

SO Sequence 295 AA;

Query Match 73.2%; Score 41; DB 4; Length 295;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
Db 110 HQWSSYPWT 118
||:| |||

RESULT 30
AAB06354
ID AAB06354 standard; peptide; 9 AA.
XX
AC AAB06354;
XX
DT 17-OCT-2000 (first entry)
XX
DE Randomised VL3 sequence of anti-VEGF antibody variant Y0241-5.
XX
XX Humanised; antibody variant; phage display; randomised library;
KW cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KW antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KW breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KW psoriasis; atherosclerosis; diabetic retinopathy;
KW complementarity determining region; CDR.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200029584-A1.
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-US027153.
XX
PR 18-NOV-1998; 98US-0108945P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen YM, Lowman HB, Muller Y;
XX
DR WPI; 2000-387797/33.
XX
PS Anticbody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.
XX
XX Example 1; Page 58; 110pp; English.
XX
CC The present sequence is the randomised VL3 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 83. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were

CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies
XX

SO Sequence 9 AA;

Query Match 71.4%; Score 40; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 17+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 OYSKLPMT 9
Db 2 QYSSVPMT 9
|||:| |||

RESULT 31
AAB06352
ID AAB06352 standard; peptide; 9 AA.
XX
AC AAB06352;
XX
DT 17-OCT-2000 (first entry)
XX
DE Randomised VL3 sequence of anti-VEGF antibody variant Y0241-3.
XX
XX Humanised; antibody variant; phage display; randomised library;
KW cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KW antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KW breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KW psoriasis; atherosclerosis; diabetic retinopathy;
KW complementarity determining region; CDR.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200029584-A1.
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-US027153.
XX
PR 18-NOV-1998; 98US-0108945P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen YM, Lowman HB, Muller Y;
XX
DR WPI; 2000-387797/33.
XX
PS Anticbody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.
XX
XX Example 1; Page 58; 110pp; English.
XX
CC The present sequence is the randomised VL3 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 83. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of

CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies

Sequence 9 AA;

Query Match 71.4%; Score 40; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QVSKLPMT 9
DB 2 QVSNVPMT 9

RESULT 32

AA030770 standard; protein; 107 AA.

AA030770;

25-MAR-2003 (revised)
12-MAY-1993 (first entry)

Consensus humanised murine anti-CD3 MAb UCHT1 VL domain hUK1.

Humanisation; rapid; monoclonal antibody; mxCd3; light chain.

Synthetic.

WO9222653-A1.

23-DEC-1992.

15-JUN-1992; 92WO-US05126.

14-JUN-1991; 91US-00715272.

(GETH) GENENTECH INC.

Carter PJ, Presta LG;

WPI, 1993-018139/02.

Humanisation of antibodies - by molecular modelling of the variable
domains and alteration by gene conversion mutagenesis.

Disclosure; Fig 5; 126p; English.

The sequence is that of a consensus sequence hUK1 of the most abundant
human subgroups, namely VL K 1 upon which is based the humanised variants
of the light chain variable domain of murine anti-CD3 monoclonal antibody
UCHT1 (mxCd3, Shalaby 1992). (Updated on 25-MAR-2003 to correct PN
field.)

Sequence 107 AA;

Query Match 71.4%; Score 40; DB 2; Length 107;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QVSKLPMT 9
DB 90 QVNSLPMT 97

RESULT 33

AA062087 standard; protein; 107 AA.

AA062087;
AC AA062087;

DT 29-MAY-2001 (first entry)
DE Human VL consensus framework hunkappal.
XX

Erbb2 receptor; anti-Erbb2 antibody; tumour; cancer; breast cancer;
KW leukemia; cytostatic; carcinoma.

Homo sapiens.

WO200115730-A1.

08-MAR-2001.

25-AUG-2000; 2000WO-US023391.

27-AUG-1999; 99US-0151018P.

23-JUN-2000; 2000US-0213822P.

(GETH) GENENTECH INC.

Baughman SA, Shak S;

WPI, 2001-235058/24.

Treating a human patient with a disorder characterized by overexpression
of Erbb2 receptor such as a tumor or cancer (e.g. metastatic breast
carcinoma) comprises administering several dosages of an anti-Erbb2
antibody.

Disclosure; Fig 5A; 71pp; English.

The invention relates to treating cancer in a human susceptible to or
diagnosed with a disorder characterized by overexpression of Erbb2
receptor. The method comprises administering an initial dose of at least
approx.5 mg/kg of the anti-Erbb2 antibody, and administering subsequent
doses of the antibody in approximately the same amount or less than the
initial dose. The method is useful for treating a disorder characterized
by overexpression of Erbb2 receptor, particularly a benign or malignant
tumour, or a cancer. The cancer is selected from breast cancer
(particularly metastatic breast carcinoma), leukemia, squamous cell
cancer, small-cell lung cancer, non-small cell lung cancer, pancreatic
cancer, gastrointestinal cancer, glioblastoma, cervical cancer, ovarian
cancer, liver cancer, bladder cancer, hepatoma, colon cancer, colorectal
cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer,
cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic
cancer, carcinoma and various types of head and neck cancer. The present sequence
represents the human variable light chain consensus framework hunkappal
(light kappa subgroup I)

Sequence 107 AA;

Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QVSKLPMT 9
DB 90 QVNSLPMT 97

RESULT 34

AA060400 standard; protein; 107 AA.

AA060400;

24-APR-2001 (first entry)

Consensus human light chain kappa subgroup I framework, SEQ ID NO:5.

Anti-Erbb2 monoclonal antibody 2C4; HER2; humanised; VL;
light chain variable region; cancer; cytostatic; EGFR-expressing cancer;
epidermal growth factor receptor; colon cancer; rectal cancer; tumour;

KW colorectal cancer; non-small cell lung cancer; metastatic breast cancer;
 XX affinity purification; kappa subgroup 1 framework.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200100245-A2.
 PN
 XX 04-JAN-2001.
 PD
 XX 23-JUN-2000; 2000WO-US017366.
 PF
 XX 25-JUN-1999; 99US-0141316P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Adams CM, Presta LG, Sliwkowsky M;
 PI WPI, 2001-080862/09.
 DR
 XX Treating cancer in a human, where the cancer expresses epidermal growth
 PT factor receptor (EGFR), comprises administering an antibody which binds
 PT ErbB2.
 PS Example 3; Fig 7A; 89pp; English.
 XX
 CC The invention relates to a method for treating cancer in a human patient,
 CC wherein the cancer expresses epidermal growth factor receptor (EGFR),
 CC comprising administering an antibody which binds ErbB2 (HER2; AAB60408).
 CC In particular, the anti-ErbB2 antibody is the murine monoclonal antibody
 CC 2C4 (AAB60396, AAB60397) or a humanised version of 2C4 (AAB60398,
 CC AAB60399). The invention also encompasses an isolated nucleic acid
 CC encoding a humanised ErbB2-binding antibody; vectors and host cells
 CC comprising such nucleic acids; the recombinant production of a humanised
 CC ErbB2-binding antibody; and an immun conjugate comprising a humanised
 CC ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies
 CC act by antagonising ErbB receptors, and as inhibitors of transforming
 CC growth factor alpha (TGF-alpha)-activated mitogen activated protein
 CC kinase (MAPK). The method of the invention is used for treating cancer,
 CC especially colon cancer, rectal cancer, colorectal cancer, lung cancer
 CC (especially non-small cell lung cancer), or breast cancer (especially
 CC metastatic breast cancer). The antibodies may also have non-therapeutic
 CC uses e.g., as affinity purification agents. Using an antibody which binds
 CC to ErbB2 to treat cancer is preferable to the use of EGFR-targeted
 CC drugs, as EGFR is also highly expressed in other tissues such as the
 CC liver and skin, where the active drug will also bind, with skin toxicity
 CC having been observed for EGFR-targeted drugs. Antibodies which bind
 CC ErbB2 are anticipated to have a better safety profile than such drugs.
 CC The present sequence represents the consensus human light chain kappa
 CC subgroup 1 framework used to humanise the anti-ErbB2 antibody 2C4
 CC
 XX Sequence 107 AA;
 SQ
 Query Match 71.4%; Score 40; DB 4; Length 107;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QYSLPMT 9
 ||:||||
 Db 90 QYNSLPMT 97
 RESULT 35
 AAB61585
 ID AAB61585 standard; protein; 107 AA.
 XX
 AC AAB61585;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human variable light chain consensus sequence.
 XX
 KW ErbB2; cytosolic; prostate cancer; receptor tyrosine kinase; human;

KW antibody; ErbB receptor; monoclonal antibody 2C4; variable light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO200100238-A1.
 XX
 PD 04-JAN-2001.
 XX
 PD 23-JUN-2000; 2000WO-US017423.
 PF
 XX 25-JUN-1999; 99US-0141315P.
 PR
 XX (GETH) GENENTECH INC.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Agus DB, Scher HI, Sliwkowski MX;
 XX WPI, 2001-159131/16.
 DR
 XX Treating prostate cancer in a human comprises administering an antibody
 PT which binds ErbB2 and blocks ligand activation of an ErbB receptor.
 PT
 XX Example 3; Fig 7; 93pp; English.
 PS
 CC The ErbB family of receptor tyrosine kinases are important mediators of
 CC cell growth, differentiation and survival. The receptor family includes
 CC four distinct members including Epidermal Growth Factor Receptor (EGFR or
 CC ErbB1), HER2 (ErbB2 or p185^{neu}), HER3 (ErbB3) and Her4 (ErbB4 or tyro2).
 CC The present invention relates to a method for treating prostate cancer.
 CC The method comprises administering an antibody which binds ErbB2 and
 CC blocks ligand activation of an ErbB receptor. Preferably, the antibody
 CC blocks binding of monoclonal antibody 2C4 to ErbB2 and/or blocks TGF-
 CC alpha activation of mitogen-activated protein kinase (MAPK). The present
 CC sequence is the consensus framework for the human variable light chain.
 CC This sequence was used in a sequence alignment homology with the variable
 CC light chain of antibody 2C4 (see AAB61581)
 CC
 XX Sequence 107 AA;
 SQ
 Query Match 71.4%; Score 40; DB 4; Length 107;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QYSLPMT 9
 ||:||||
 Db 90 QYNSLPMT 97
 RESULT 36
 ADE71454
 ID ADE71454 standard; protein; 107 AA.
 XX
 AC ADE71454;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human antibody variable light chain framework.
 XX
 KW Cytostatic; ErbB2 antagonist; tyrosine kinase inhibitor; cancer; ErbB2;
 KW ErbB2 antibody; carcinoma; lymphoma; blastoma; sarcoma; liposarcoma;
 KW neuroendocrine tumour; mesothelioma; schwannoma; meningioma;
 KW adenocarcinoma; melanoma; leukaemia; lymphoid malignancy;
 KW squamous cell cancer; epithelial squamous cell cancer; lung cancer;
 KW small-cell lung cancer; non-small cell lung cancer;
 KW adenocarcinoma of the lung; squamous carcinoma of the lung;
 KW cancer of the peritoneum; hepatocellular cancer; gastric cancer;
 KW stomach cancer; gastrointestinal cancer; pancreatic cancer; glioblastoma;
 KW cervical cancer; ovarian cancer; liver cancer; bladder cancer; hepatoma;
 KW breast cancer; colon cancer; rectal cancer; colorectal cancer;
 KW endometrial carcinoma; uterine carcinoma; salivary gland carcinoma;
 KW kidney cancer; renal cancer; prostate cancer; vulval cancer;
 KW thyroid cancer; hepatic carcinoma; anal carcinoma; penile carcinoma;
 KW testicular cancer; oesophageal cancer; tumour of the biliary tract;

XX head and neck cancer; human antibody; variable light chain framework.
XX
OS Homo sapiens.
XX
PN US2003086924-A1.
XX
PD 08-MAY-2003.
XX
PF 10-OCT-2002; 2002US-00268501.
XX
PR 25-JUN-1999; 99US-0141316P.
XX
PR 23-JUN-2000; 2000US-00602812.
XX
PA (GETH) GENENTECH INC.
XX
PI Sliwowski MX;
XX
XX WPI; 2004-020226/02.
XX
PT Treating cancer (e.g. carcinoma, lymphoma or sarcoma) that expresses
XX optionally an epidermal growth factor receptor-targeted drug or a
XX tyrosine kinase inhibitor.
XX
XX Example 3; SEQ ID NO 5; 56pp; English.
XX
XX The invention describes a method of treating cancer that expresses ErbB2
XX comprising administering to a patient an antibody that binds ErbB2.
XX Specifically claimed are antibodies that bind ErbB2, particularly
XX monoclonal antibody 2C4 or humanised 2C4, or monoclonal antibody 4D5 or
XX humanised 4D5. The methods are useful for treating cancer in a patient,
XX particularly a human. The cancer includes carcinoma, lymphoma, blastoma,
XX sarcoma, liposarcoma, neuroendocrine tumour, mesothelioma, schwannoma,
XX meningioma, adenocarcinoma, melanoma, leukaemia, lymphoid malignancy,
XX squamous cell cancer, epithelial squamous cell cancer, lung cancer, small
XX cell lung cancer, non-small cell lung cancer, adenocarcinoma of the
XX lung, squamous carcinoma of the lung, cancer of the peritoneum,
XX hepatocellular cancer, gastric or stomach cancer, gastrointestinal
XX cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer,
XX liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer,
XX rectal cancer, colorectal cancer, endometrial or uterine carcinoma,
XX salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval
XX cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile
XX carcinoma, testicular cancer, esophageal cancer, a tumour of the biliary
XX tract, or head and neck cancer. This is the amino acid sequence of human
XX antibody variable light chain framework that was used to produce a
XX humanised antibody.
XX
XX Sequence 107 AA:
XX
XX Query Match 71.4%; Score 40; DB 8; Length 107;
XX Best Local Similarity 75.0%; Pred. No. 28;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
XX
XX 2 QYSLPWT 9
XX ||: ||||
XX 90 QYNSLPWT 97
XX
XX RESULT 37
XX ID ADJ88008
XX ADJ88008 standard; protein; 107 AA.
XX
XX ADJ88008;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human variable light chain consensus peptide.
XX
XX Cancer; ErbB2; gene therapy; human.
XX
XX Homo sapiens.
XX
XX Unidentified.
XX

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XX PN US2004013667-A1.
XX PD
XX PD 22-JAN-2004.
XX PF
XX PF 27-JUN-2003; 2003US-00608626.
XX XX
XX PR 25-JUN-1999; 99US-0141316P.
XX PR 23-JUN-2000; 2000US-00602812.
XX PR 10-OCT-2002; 2002US-00268501.
XX PA (GETH ) GENENTECH INC.
XX PI Kelsey SM, Sliwkowski MX;
XX DR
XX DR WPI; 2004-121529/12.
XX PT Treating cancer that expresses ErbB2 e.g., breast, colon, rectal or
XX PT colorectal cancer comprises administering an antibody that binds to ErbB2
XX PT to a patient.
XX PS
XX PS Example 3; SEQ ID NO 5; 56pp; English.
XX CC
XX CC The present invention relates to methods for treating cancer such as
XX CC carcinoma, lymphoma, blastoma, medulloblastoma, retinoblastoma, sarcoma,
XX CC liposarcoma, synovial cell sarcoma, neuroendocrine tumour, carcinoid
XX CC tumour, gastrinoma, islet cell cancer, mesothelioma, schwannoma, acoustic
XX CC neuroma, meningioma, adenocarcinoma, melanoma, leukaemia, lymphoid
XX CC malignancy, squamous cell cancer, epithelial squamous cell cancer, lung
XX CC cancer, small-cell lung cancer, non-small cell lung cancer,
XX CC adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the
XX CC peritoneum, hepatocellular cancer, gastric or stomach cancer,
XX CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
XX CC cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast
XX CC cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or
XX CC uterine carcinoma, salivary gland carcinoma, kidney or renal cancer,
XX CC prostate cancer, vulvar cancer, thyroid cancer, hepatic carcinoma, anal
XX CC carcinoma, penile carcinoma, testicular cancer, oesophageal cancer, a
XX CC tumour of the biliary tract or head and neck cancer with anti-ErbB2
XX CC antibodies. The invention is also useful in gene therapy. The present
XX CC sequence is human variable light chain consensus peptide.
XX SQ
XX SQ Sequence 107 AA;
XX
XX Query Match 71.4%; Score 40; DB: 8; Length 107;
XX Best Local Similarity 75.0%; Pred. No. 28;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 QYSLPWT 9
XX ||: |||||
XX Db 90 QYNSLPWT 97
XX
XX RESULT 38
XX ID ADN12054 standard; protein; 107 AA.
XX ADN12054;
XX AC ADN12054;
XX XX
XX XX 17-JUN-2004 (first entry)
XX DT
XX XX
XX DE Variable light chain consensus sequence.
XX XX
XX KW tumor; anti-HER2 antibody; HER2/HER3; HER2/HER1; Cytostatic; cancer.
XX OS Homo sapiens.
XX XX
XX PN WO200400809-A2.
XX PD
XX PD 22-JAN-2004.
XX XX
XX XX 11-JUN-2003; 2003WO-US021590.
XX PF
XX

```

PR 15-JUL-2002; 2002US-0396290P.
 PR 20-JUN-2003; 2003US-0480043P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Koll H, Bossemmaier B, Mueller H, Sliwkowski MX, Kelsey SM,
 XX WPI; 2004-156546/15.
 DR
 XX Identifying a tumor responsive to treatment with an anti-HER2 antibody,
 PT useful in treating cancer, comprises detecting the presence of a
 PT HER2/HER3 and/or HER2/HER1 protein complex.
 XX
 PS Disclosure; SEQ ID NO 5; 105pp; English.
 XX
 CC The present invention relates to identifying a tumor responsive to
 CC treatment with an anti-HER2 antibody involves detecting the presence of
 CC an HER2/HER3 and/or HER2/HER1 protein complex in a sample of the tumor.
 CC The method is useful in identifying a tumor as responsive to treatment
 CC with an anti-HER2 antibody. The methods and antibodies are useful in
 CC treating a condition or disorder including tumor or cancer, e.g. breast,
 CC prostate, lung, colorectal or ovarian cancer. The present sequence
 CC represents a variable light chain consensus sequence.

XX
 SQ Sequence 107 AA;

Query Match 71.4%; Score 40; DB 8; Length 107;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
 ||: ||||
 Db 90 QYNSLPWT 97

RESULT 39

ADP43328
 ID ADP43328 standard; protein; 107 AA.

XX
 AC ADP43328;

XX
 DT 26-AUG-2004 (first entry)

XX
 DE Human monoclonal variable light kappa chain antibody SegID 5.

XX human; variable light kappa chain; antibody;
 KM epidermal growth factor receptor; ErbB; ErbB2;
 KM transforming growth factor alpha; benign hyperproliferative disorder;
 KM psoriasis; endometriosis; scleroderma; vascular disease; atherosclerosis;
 KM restenosis; colon polyps; fibroadenoma; respiratory disease;
 KM chronic bronchitis; cystic fibrosis; cytostatic; antipsoriatic;
 KM gynaecological; dermatological; vasotrophic; antiarteriosclerotic;
 KM cardiant; antianginal; antihypertensive; antidiabetic; antidiabetic;
 KM anti-allergic; anti-inflammatory; antitussive.

XX
 OS Homo sapiens.

XX
 PN WO2004048525-A2.

XX
 PD 10-JUN-2004.

XX
 PF 21-NOV-2003; 2003WO-US037367.

XX
 PR 21-NOV-2002; 2002US-0428027P.

XX
 PA (GETH) GENENTECH INC.

XX
 PI Sliwkowski MX, Brunetta FG;

XX
 DR WPI; 2004-450361/42.

XX
 PT Treating non-malignant disease or disorder such as psoriasis, epidermal
 PT endometriosis, involving abnormal activation or production of epidermal

PT growth factor receptor or ErbB ligand by administering antibody that
 PT binds ErbB2 to mammal.

XX
 PS Example 3; SEQ ID NO 5; 74pp; English.

XX
 CC This invention refers to a novel method for treating a non-malignant
 CC disease that involves abnormal activation or production of an epidermal
 CC growth factor receptor (ErbB) receptor or an ErbB ligand. Specifically,
 CC it refers to the use of humanised murine anti-ErbB2 antibodies to block
 CC ligand activation of the ErbB receptor, where the ErbB ligand is a
 CC transforming growth factor alpha that promotes mitogen-activated protein
 CC kinase (MAPK). The present invention describes conjugating the monoclonal
 CC murine antibody 2C4, or more particularly the humanised antibody 574, to
 CC a cytotoxic or therapeutic agent such that it can be used to treat a
 CC benign hyperproliferative disorder, psoriasis, endometriosis,
 CC scleroderma, vascular disease (such as atherosclerosis or restenosis),
 CC colon polyps, fibroadenoma or respiratory disease (such as chronic
 CC bronchitis or cystic fibrosis). Accordingly, they exhibit cytostatic,
 CC antipsoriatic, gynaecological, dermatological, vasotrophic, hypotensive,
 CC antiarteriosclerotic, cardiant, antianginal, antidiabetic, antipsoriatic,
 CC antiasthmatic, anti-allergic, anti-inflammatory and antitussive activities.
 CC This polypeptide sequence is the human variable light kappa chain protein
 CC used to humanise the murine anti-ErbB2 proteins of the invention.

XX
 SQ Sequence 107 AA;

Query Match 71.4%; Score 40; DB 8; Length 107;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
 ||: ||||
 Db 90 QYNSLPWT 97

RESULT 40

AAW04177
 ID AAW04177 standard; protein; 108 AA.

XX
 AC AAW04177;

XX
 DT 19-MAY-1997 (first entry)

XX
 DE Variant variable light chain of Fas ligand antibody NOK-1.

XX
 KM Variable region; light chain; human; Fas ligand; monoclonal; antibody;
 KM NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
 KM hepatitis; infectious mononucleosis; systemic lupus erythematosus;
 KM variant.

XX
 OS Mus musculus.

XX
 PN WO9629350-A1.

XX
 PD 26-SEP-1996.

XX
 PF 21-MAR-1996; 96WO-JP000734.

XX
 PR 20-MAR-1995; 95JP-00087420.

XX
 PR 27-OCT-1995; 95JP-00303492.

XX
 PA (SUME) SUMITOMO ELECTRIC IND CO.

XX
 PI Kayagaki N, Yagita H, Okumura K, Nakata M;

XX
 DR WPI; 1996-443140/44.

XX
 DR N-PADB; AAT39350.

XX
 PT Monoclonal antibody specifically recognising the Fas ligand - useful for
 PT the detection of Fas ligands either on cell surface or in solution.

XX
 PS Claim 20; Page 80-81; 133pp; Japanese.

CC The present sequence is a variant light chain variable region of the anti
CC -human Fas ligand monoclonal antibody (Mab) NOK-1. NOK-1 is produced by
CC the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
CC with transformed human Fas ligand expressing COS cells, and fusing spleen
CC cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
CC cells. The Mab recognises the human Fas ligand on the cell surface or in
CC solution, and can be used to inhibit the apoptosis inducing cell surface
CC Fas ligand/Fas reaction. The Mab can also be used for a Fas ligand assay
CC in biological samples (e.g. human blood), especially for disease
CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
CC erythematosus.

XX Sequence 108 AA;

Query Match 71.4%; Score 40; DB 2; Length 108;

Best Local Similarity 75.0%; Pred. No. 29;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

Db 90 QYSEFPWT 97

Search completed: December 17, 2004, 18:29:07
Job time : 29.3539 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 16:13:27 ; Search time 5.46067 seconds
(without alignments)
109.302 Million cell updates/sec

Title: US-10-089-500-8
Perfect score: 56
Sequence: 1 HQYSKLPMW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/prodata/1/aa/6A_COMB.pep:*
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5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	128	4	US-09-225-322B-10
2	56	100.0	128	4	US-09-225-322B-19
3	56	100.0	128	4	US-09-764-304-10
4	56	100.0	128	4	US-09-764-304-19
5	40	71.4	9	4	US-09-440-781-24
6	40	71.4	9	4	US-09-440-781-26
7	40	71.4	107	2	US-07-934-373C-18
8	40	71.4	107	3	US-08-437-642B-18
9	40	71.4	107	4	US-08-146-067C-18
10	40	71.4	107	4	US-09-648-067A-14
11	40	71.4	107	4	US-09-705-686-18
12	40	71.4	107	4	US-09-705-922A-18
13	40	71.4	107	5	PCT-US93-07832-18
14	40	71.4	108	3	US-08-974-899-3
15	40	71.4	108	3	US-09-065-059-3
16	40	71.4	108	4	US-09-795-798-3
17	39	69.6	9	2	US-08-560-558B-31
18	39	69.6	9	4	US-09-217-268B-31
19	39	69.6	9	4	US-09-440-781-25
20	39	69.6	110	4	US-09-440-781-94
21	39	69.6	110	4	US-09-440-781-95
22	39	69.6	113	1	US-08-497-112-18
23	39	69.6	114	2	US-08-560-558B-27
24	39	69.6	114	4	US-09-217-268B-27
25	39	69.6	114	4	US-09-217-268B-35
26	39	69.6	116	1	US-08-497-312-14
27	38	67.9	191	4	US-09-270-767-37260

28	38	67.9	191	4	US-09-270-767-52477	Sequence 52477, A
29	38	67.9	249	2	US-08-797-689-18	Sequence 18, Appl
30	38	67.9	249	4	US-09-984-186-18	Sequence 4, Appl
31	38	67.9	572	6	5200183-5	Patent No. 5200183
32	38	67.9	573	6	5215909-12	Patent No. 5215909
33	38	67.9	602	3	US-08-446-100-1	Sequence 1, Appl
34	38	67.9	602	3	US-08-446-100-2	Sequence 2, Appl
35	38	67.9	602	3	US-08-446-100-3	Sequence 3, Appl
36	38	67.9	602	3	US-08-446-100-4	Sequence 4, Appl
37	38	67.9	602	3	US-08-446-100-5	Sequence 5, Appl
38	38	67.9	602	3	US-08-446-100-6	Sequence 6, Appl
39	38	67.9	602	3	US-08-446-100-7	Sequence 7, Appl
40	38	67.9	602	3	US-08-446-100-8	Sequence 8, Appl
41	38	67.9	602	3	US-08-446-100-9	Sequence 9, Appl
42	38	67.9	602	3	US-08-446-100-10	Sequence 10, Appl
43	38	67.9	602	3	US-08-446-100-11	Sequence 11, Appl
44	38	67.9	602	3	US-08-446-100-12	Sequence 12, Appl
45	38	67.9	602	3	US-08-446-100-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAI, HIROMASA
; APPLICANT: KOMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-10

Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 HQYSKLPMW 9
Db      109 HQYSKLPMW 117

RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO

```

```
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/225,322B
/ CURRENT FILING DATE: 1999-01-05
/ PRIOR APPLICATION NUMBER: US 08/454,680
/ PRIOR FILING DATE: 1995-05-31
/ PRIOR APPLICATION NUMBER: US 08/408,133
/ PRIOR FILING DATE: 1995-03-21
/ PRIOR APPLICATION NUMBER: US 08/292,178
/ PRIOR FILING DATE: 1994-08-17
/ PRIOR APPLICATION NUMBER: US07/947,674
/ PRIOR FILING DATE: 1992-09-17
/ PRIOR APPLICATION NUMBER: JP 3-238375
/ PRIOR FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:light chain
/ US-09-225-322B-19

Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117

RESULT 3
US-09-764-304-10
/ Sequence 10, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: CDNA KM-641
/ US-09-764-304-10
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Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117

RESULT 4
US-09-764-304-19
/ Sequence 19, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain
/ US-09-764-304-19

Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117

RESULT 5
US-09-440-781-24
/ Sequence 24, Application US/09440781
/ Patent No. 6632926
/ GENERAL INFORMATION:
/ APPLICANT: Yvonne Man-yea Chen et al.
/ TITLE OF INVENTION: ANTIBODY VARIANTS
/ FILE REFERENCE: P1469R1
/ CURRENT APPLICATION NUMBER: US/09/440,781
/ CURRENT FILING DATE: 1999-11-16
/ NUMBER OF SEQ ID NOS: 99
/ SEQ ID NO 24
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ NAME/KEY: artificial
/ LOCATION: 1-9
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OTHER INFORMATION: variant CDR sequence
US-09-440-781-24

Query Match 71.4%; Score 40; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
Db 2 QYSLPMT 9

RESULT 6
US-09-440-781-26

Sequence 26, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 26
LENGTH: 9
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-9
OTHER INFORMATION: variant CDR sequence
US-09-440-781-26

Query Match 71.4%; Score 40; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
Db 2 QYSLPMT 9

RESULT 7
US-07-934-373C-18

Sequence 18, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/715272
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-18

Query Match 71.4%; Score 40; DB 2; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
Db 90 QYSLPMT 97

RESULT 8
US-08-437-642B-18

Sequence 18, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-18

Query Match 71.4%; Score 40; DB 3; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 9
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146.206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-18

Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 10
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ExB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/09/648.067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018

; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 11
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6638055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705.686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 12
US-09-705-392A-18
Sequence 18, Application US/09705392A
Patent No. 671971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-No. 671971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18
Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 QVSKLPWT 9
DB 90 QVNSLPWT 97
RESULT 13
PCT-US93-07832-18
Sequence 18, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: Linear
PCT-US93-07832-18
Query Match 71.4%; Score 40; DB 5; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 QVSKLPWT 9
DB 90 QVNSLPWT 97
RESULT 14
US-08-974-899-3
Sequence 3, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-974-899-3

Query Match 71.4%; Score 40; DB 3; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
||:||||
DB 90 QYNSLPWT 97

RESULT 15
US-09-065-059-3
; Sequence 3, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:

APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-065-059-3

Query Match 71.4%; Score 40; DB 3; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
||:||||
DB 90 QYNSLPWT 97

RESULT 16
US-09-795-798-3
; Sequence 3, Application US/09795798

Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipain (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-795-798-3
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 71.4%; Score 40; DB 4; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
||:||||
DB 90 QYNSLPWT 97

RESULT 17
US-08-560-558E-31
; Sequence 31, Application US/08560558E
; Patent No. 5891996
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Humanized and chimeric monoclonal
; antibodies that recognize epidermal growth factor receptor
; TITLE OF INVENTION: BGF-R; diagnostic and therapeutic use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
; STREET: P.O. Box 2250
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: United States of America
; ZIP: 84110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS95
SOFTWARE: Wordperfect 5.1/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E

FILING DATE: No. 5891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2720US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
TELEFAX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-560-558B-31

Query Match 69.6%; Score 39; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPMT 9
DB 2 QYSHVPMT 9

RESULT 18
US-09-217-268B-31
Sequence 31, Application US/09217268B
Patent No. 6506883
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriguez, Rolando P
APPLICANT: Frias, Ernesto M
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
FILE REFERENCE: 2720.1US
CURRENT APPLICATION NUMBER: US/09/217,268B
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Murine
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-31

Query Match 69.6%; Score 39; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPMT 9
DB 2 QYSHVPMT 9

RESULT 19
US-09-440-781-25
Sequence 25, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 25
LENGTH: 9

TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-9
OTHER INFORMATION: variant CDR sequence
US-09-440-781-25

Query Match 69.6%; Score 39; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPMT 9
DB 2 QYSHVPMT 9

RESULT 20
US-09-440-781-94
Sequence 94, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match 69.6%; Score 39; DB 4; Length 110;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPMT 9
DB 90 QYSHVPMT 97

RESULT 21
US-09-440-781-95
Sequence 95, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 95
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match 69.6%; Score 39; DB 4; Length 110;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPMT 9

Db 90 QYSHVPT 97

RESULT 22

US-08-497-312-18
; Sequence 18, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATABEY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,312
; FILING DATE: 30-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: CU 80/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 2629US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEEX: 388961 1PM04UT
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-08-497-312-18

Query Match 69.6%; Score 39; DB 1; Length 113;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSHVPT 9
Db 95 QYSHVPT 102

RESULT 23

US-08-560-558E-27
; Sequence 27, Application US/08560558E
; Patent No. 5891996
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Humanized and chimeric monoclonal
; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
; TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
; STREET: P.O. Box 2250
; CITY: Salt Lake City

STATE: Utah
COUNTRY: United States of America
ZIP: 84110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Wordperfect 5.1/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E
FILING DATE: No. 5891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2720US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
TELEFAX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-560-558E-27

Query Match 69.6%; Score 39; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSHVPT 9
Db 95 QYSHVPT 102

RESULT 24
US-09-217-268B-27
; Sequence 27, Application US/09217268B
; Patent No. 6506883
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies that Recognize Epider
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
; FILE REFERENCE: 2720.1US
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 27
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Murine R3 antibody
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Deduced amino acid sequence of VK of murine R3 antibody
US-09-217-268B-27

Query Match 69.6%; Score 39; DB 4; Length 114;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSHVPT 9
Db 95 QYSHVPT 102

RESULT 25

US-09-217-268B-35
; Sequence 35, Application US/09217268B

Patent No. 6506883
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriguez, Rolando P
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
FILE REFERENCE: 2720.1US
CURRENT APPLICATION NUMBER: US/09/217,268B
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 114
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of humanized VK of murine R3 antibody contain
US-09-217-268B-35

Query Match
Best Local Similarity 69.6%; Score 39; DB 4; Length 114;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXSKLPMT 9
DB 95 QYSHVPM 102

RESULT 26
US-08-497-312-14
Sequence 14, Application US/08497312
Patent No. 572120
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PMO4UT
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein

HYPOTHETICAL: NO
US-08-497-312-14

Query Match
Best Local Similarity 69.6%; Score 39; DB 1; Length 116;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXSKLPMT 9
DB 97 QYSHVPM 104

RESULT 27
US-09-270-767-37260
Sequence 37260, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37260
LENGTH: 191
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-37260

Query Match
Best Local Similarity 67.9%; Score 38; DB 4; Length 191;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
DB 147 HRYSQRPM 155

RESULT 28
US-09-270-767-52477
Sequence 52477, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52477
LENGTH: 191
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52477

Query Match
Best Local Similarity 67.9%; Score 38; DB 4; Length 191;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
DB 147 HRYSQRPM 155

RESULT 29
US-08-797-689-18
Sequence 18, Application US/08797689

Patent No. 5876969
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTRAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-797-689-18

Query Match 67.9%; Score 38; DB 2; Length 249;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 232 QYSSYPWT 239

RESULT 30
US-09-984-186-18
Sequence 18, Application US/0994186
Patent No. 6686179
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-984-186-18

Query Match 67.9%; Score 38; DB 4; Length 249;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 232 QYSSYPWT 239

RESULT 31
5200183-5
Patent No. 5200183
APPLICANT: TANG, JORDAN J N; WANG, CHI-SUN
TITLE OF INVENTION: RECOMBINANT BLUE SALT ACTIVATED LIPASES
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,426
FILING DATE: 12-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 504,635
FILING DATE: 04-APR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO: 5:
LENGTH: 572
5200183-5

Query Match 67.9%; Score 38; DB 6; Length 572;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8

Db 421 HRSSKLPW 428

RESULT 32

5215909-12
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:12
; LENGTH: 573
5215909-12

Query Match 67.9%; Score 38; DB 6; Length 573;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYSKLPW 8
Db 424 HRSSKLPW 431

RESULT 33

US-08-446-100-1
; Sequence 1, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES

; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-1

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYSKLPW 8
Db 451 HRSSKLPW 458

RESULT 34

US-08-446-100-2
; Sequence 2, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: human esterases
US-08-446-100-2

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYSKLPW 8
Db 451 HRSSKLPW 458

RESULT 35

US-08-446-100-3
; Sequence 3, Application US/08446100

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; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-3
;
Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
|:|||||
Db 451 HRSSKLPW 458

RESULT 36
US-08-446-100-4
; Sequence 4, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-4
;
Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
|:|||||
Db 451 HRSSKLPW 458

RESULT 37
US-08-446-100-5
; Sequence 5, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
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STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-5

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 451 HRSSKLPW 458

RESULT 38
US-08-446-100-6
Sequence 6, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-6

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 451 HRSSKLPW 458

RESULT 39
US-08-446-100-7
Sequence 7, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-7

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 451 HRSSKLPW 458

RESULT 40
US-08-446-100-8
Sequence 8, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA

COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEetical: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-8

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
|: |||||
Db 451 HRSSKLPW 458

Search completed: December 17, 2004, 18:32:10
Job time : 6.46067 secs

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OM protein - protein search, using SW model

Run on: December 17, 2004, 18:20:33 ; Search time 17.3933 seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQYSKLPWT 9

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Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	56	100.0	128 9 US-09-764-304-10	Sequence 10, Appl
2	56	100.0	128 9 US-09-764-304-19	Sequence 19, Appl
3	56	100.0	128 14 US-10-265-713-10	Sequence 10, Appl
4	56	100.0	128 14 US-10-265-713-19	Sequence 19, Appl
5	56	100.0	128 14 US-10-166-626-10	Sequence 10, Appl
6	56	100.0	128 14 US-10-166-626-19	Sequence 19, Appl
7	44	78.6	99 16 US-10-371-942-6	Sequence 6, Appl1
8	44	78.6	109 14 US-10-371-942-32	Sequence 32, Appl1
9	43	76.8	215 15 US-10-264-049-4290	Sequence 4290, Ap
10	40	71.4	9 15 US-10-624-153-24	Sequence 24, Appl
11	40	71.4	9 15 US-10-624-153-26	Sequence 26, Appl
12	40	71.4	93 15 US-10-424-599-159861	Sequence 159861,
13	40	71.4	107 14 US-10-268-501-5	Sequence 5, Appl1

ALIGNMENTS

14	40	71.4	107	15	US-10-608-626-5	Sequence 5, Appl1
15	40	71.4	107	15	US-10-600-152-14	Sequence 14, Appl
16	40	71.4	107	16	US-10-619-754-5	Sequence 5, Appl1
17	40	71.4	107	17	US-10-835-641-18	Sequence 18, Appl
18	40	71.4	108	9	US-09-056-1608-12	Sequence 12, Appl
19	40	71.4	108	10	US-09-795-798-3	Sequence 3, Appl1
20	40	71.4	108	14	US-10-234-671-12	Sequence 12, Appl
21	40	71.4	109	9	US-09-811-123-6	Sequence 6, Appl1
22	40	71.4	110	14	US-10-044-896-4	Sequence 4, Appl1
23	40	71.4	126	16	US-10-469-125-8	Sequence 8, Appl1
24	40	71.4	153	9	US-09-187-693-62	Sequence 62, Appl
25	40	71.4	159	9	US-09-187-693-66	Sequence 66, Appl
26	39	69.6	9	9	US-09-056-1608-6	Sequence 6, Appl1
27	39	69.6	9	9	US-09-217-2608-31	Sequence 31, Appl1
28	39	69.6	9	14	US-10-234-671-6	Sequence 6, Appl1
29	39	69.6	9	15	US-10-624-153-25	Sequence 25, Appl
30	39	69.6	64	17	US-10-425-115-293070	Sequence 293070,
31	39	69.6	103	16	US-10-379-392-100	Sequence 100, App
32	39	69.6	103	16	US-10-379-392-121	Sequence 121, App
33	39	69.6	103	16	US-10-379-392-123	Sequence 123, App
34	39	69.6	103	16	US-10-379-392-129	Sequence 129, App
35	39	69.6	103	16	US-10-379-392-131	Sequence 131, App
36	39	69.6	107	9	US-09-056-1608-13	Sequence 13, Appl
37	39	69.6	107	9	US-09-056-1608-15	Sequence 15, Appl
38	39	69.6	107	14	US-10-234-671-13	Sequence 13, Appl
39	39	69.6	107	14	US-10-234-671-15	Sequence 14, Appl
40	39	69.6	107	14	US-10-251-215-49	Sequence 49, Appl
41	39	69.6	107	16	US-10-723-434-1	Sequence 1, Appl1
42	39	69.6	107	16	US-10-723-434-2	Sequence 2, Appl1
43	39	69.6	107	16	US-10-723-434-3	Sequence 3, Appl1
44	39	69.6	107	16	US-10-723-434-4	Sequence 4, Appl1
45	39	69.6	107	16	US-10-723-434-5	Sequence 5, Appl1

RESULT 1
US-09-764-304-10

Sequence 10, Application US/09764304

Patent No. US2002026036A1

GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA

APPLICANT: HANAI, NOBUO

APPLICANT: HASEGAWA, MAMORU

APPLICANT: MIYAJI, HIROMASA

APPLICANT: KUMANA, YOSHITISHA

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY

FILE REFERENCE: 249-101

CURRENT APPLICATION NUMBER: US/09/764,304

EARLIER FILING DATE: 2001-01-19

EARLIER APPLICATION NUMBER: 09/225,332

EARLIER FILING DATE: 1999-01-05

EARLIER APPLICATION NUMBER: US 08/454,680

EARLIER FILING DATE: 1995-05-31

EARLIER APPLICATION NUMBER: US 08/408,133

EARLIER FILING DATE: 1995-03-21

EARLIER APPLICATION NUMBER: US 08/292,178

EARLIER FILING DATE: 1994-08-17

EARLIER APPLICATION NUMBER: US07/947,674

EARLIER FILING DATE: 1992-09-17

EARLIER APPLICATION NUMBER: JP 3-238375

EARLIER FILING DATE: 1991-09-18

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 128

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: CDNA KM-641

US-09-764-304-10

Query Match 100.0%; Score 56; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117

RESULT 2

US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 100.0%; Score 56; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117

RESULT 3

US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31

; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117

RESULT 4

US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-265-713-19

Query Match 100.0%; Score 56; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117


```
RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US2003016876A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-166-626-10
Query Match      100.0%; Score 56; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPMT 9
Db      109 HOYSKLPMT 117

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US2003016876A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
```

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; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-166-626-19
Query Match      100.0%; Score 56; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPMT 9
Db      109 HOYSKLPMT 117

RESULT 7
US-10-697-399-6
; Sequence 6, Application US/10697399
; Publication No. US20040162413A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Vassero, Alain P.
; APPLICANT: Marquis, David P.
; APPLICANT: Smith, Eric P.
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-08122
; CURRENT APPLICATION NUMBER: US/10/697,399
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-697-399-6
Query Match      78.6%; Score 44; DB 16; Length 99;
Best Local Similarity 87.5%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPMT 9
Db      82 QYSKLPMT 89

RESULT 8
US-10-371-942-32
; Sequence 32, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renertus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-32
Query Match      78.6%; Score 44; DB 14; Length 109;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 HQSKLPWT 9
|||
Db 90 HQYGFLPWT 98

RESULT 9
US-10-264-049-4290
; Sequence 4290, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 4290
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4290

Query Match 76.8%; Score 43; DB 15; Length 215;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPWT 9
|||||
Db 196 YSKLPWT 202

RESULT 10
US-10-624-153-24
; Sequence 24, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTI-BODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-9
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-24

Query Match 71.4%; Score 40; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
|||: |||
Db 2 QYSSVPWT 9

RESULT 11
US-10-624-153-26
; Sequence 26, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTI-BODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: artificial
; LOCATION: 1-9
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-26

Query Match 71.4%; Score 40; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
|||: |||
Db 2 QYSSVPWT 9

RESULT 12
US-10-424-599-159861
; Sequence 159861, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 159861
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_115373C.1.pcp
US-10-424-599-159861

Query Match 71.4%; Score 40; DB 15; Length 93;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 56 HRLQKLEPWT 64

RESULT 13

US-10-268-501-5

Sequence 5, Application US/10268501

Publication No. US20030086924A1

GENERAL INFORMATION:

APPLICANT: Sliwkowski, Mark X.

TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies

FILE REFERENCE: P1467R2P1

CURRENT APPLICATION NUMBER: US/10/268,501

PRIOR FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 09/602,812

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/141,316

PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 5

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: light chain consensus sequence

US-10-268-501-5

Query Match

Best Local Similarity 71.4%; Score 40; DB 14; Length 107;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9

Db 90 QYNSLPWT 97

RESULT 14

US-10-608-626-5

Sequence 5, Application US/10608626

Publication No. US20040013667A1

GENERAL INFORMATION:

APPLICANT: Kelsey, Stephen M.

APPLICANT: Sliwkowski, Mark X.

TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies

FILE REFERENCE: P1467R2P2

CURRENT APPLICATION NUMBER: US/10/608,626

PRIOR FILING DATE: 2003-06-27

PRIOR APPLICATION NUMBER: US 10/268,501

PRIOR FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 09/602,812

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/141,316

PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 5

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: light chain consensus sequence

US-10-608-626-5

Query Match

Best Local Similarity 71.4%; Score 40; DB 15; Length 107;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9

Db 90 QYNSLPWT 97

RESULT 15

US-10-600-152-14

Sequence 14, Application US/10600152

Publication No. US20040037824A1

GENERAL INFORMATION:

APPLICANT: Baughman, Sharon A.

APPLICANT: Shak Steven

TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies

FILE REFERENCE: P1775R1

CURRENT APPLICATION NUMBER: US/10/600,152

PRIOR FILING DATE: 2003-06-20

PRIOR APPLICATION NUMBER: 09/648,067

PRIOR FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/151,018

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: US 60/213,822

PRIOR FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 14

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: VL consensus sequence

US-10-600-152-14

Query Match

Best Local Similarity 71.4%; Score 40; DB 15; Length 107;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9

Db 90 QYNSLPWT 97

RESULT 16

US-10-619-754-5

Sequence 5, Application US/10619754

Publication No. US20040106161A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Koll, Hans

APPLICANT: Bosenmaier, Birgit

APPLICANT: Muller, Hans-Joachim

APPLICANT: Sliwkowski, Mark

TITLE OF INVENTION: Methods For Identifying Tumors That Are Responsive To Treatment With Anti-ErbB2 Antibodies

FILE REFERENCE: 39766-011A

CURRENT APPLICATION NUMBER: US/10/619,754

PRIOR FILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: US 60/396,290

PRIOR FILING DATE: 2002-07-15

PRIOR APPLICATION NUMBER: US 60/480,043

PRIOR FILING DATE: 2003-06-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 107

TYPE: PRT

ORGANISM: Homo sapiens

US-10-619-754-5

Query Match

Best Local Similarity 71.4%; Score 40; DB 16; Length 107;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9

Db 90 QYNSLPWT 97

RESULT 17

US-10-835-641-18

Sequence 18, Application US/10835641

Publication No. US20040236078A1

GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/835,641
FILING DATE: 30-Apr-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-Nov-2000
APPLICATION NUMBER: 08/146206
FILING DATE: 17-Nov-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-Jun-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-835-641-18

Query Match 71.4%; Score 40; DB 17; Length 107;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 18
US-09-056-160B-12
Sequence 12, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-12

Query Match 71.4%; Score 40; DB 9; Length 108;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 19
US-09-795-798-3
Sequence 3, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-795-798-3

Query Match 71.4%; Score 40; DB 10; Length 108;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 20
US-10-234-671-12

Sequence 12, Application US/10234671
Publication No. US20030190317A1

GENERAL INFORMATION:
APPLICANT: Baca, Manuel

Wellis, James A.
Presta, Leonard G.
Lowman, Henry B.

Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco

STATE: California

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998

APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids

TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-234-671-12

Query Match 71.4%; Score 40; DB 14; Length 108;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 21
US-09-811-123-6

Sequence 6, Application US/09811123
Patent No. US20020001587A1

GENERAL INFORMATION:

APPLICANT: Sharon Erickson

APPLICANT: Ralph Schwall

APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERB

FILE REFERENCE: GENENT. 073A2
CURRENT APPLICATION NUMBER: US/09/811,123

CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327

PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 09/602,530

PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6

LENGTH: 109

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Humanized Antibody Sequence

US-09-811-123-6

Query Match 71.4%; Score 40; DB 9; Length 109;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 22
US-10-044-896-4

Sequence 4, Application US/10044896
Publication No. US20030166228A1

GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan

APPLICANT: Kim, Jin K.

APPLICANT: Stewart, Timothy

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
FILE REFERENCE: GENENT. 074A

CURRENT APPLICATION NUMBER: US/10/044,896
CURRENT FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: 60/270775
PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4
LENGTH: 110

TYPE: PRT
ORGANISM: Homo sapiens

US-10-044-896-4
Query Match 71.4%; Score 40; DB 14; Length 110;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 23
US-10-469-125-8

Sequence 8, Application US/10469125
Publication No. US20040143101A1

GENERAL INFORMATION:
APPLICANT: Solitis, Daniel A.

APPLICANT: Burch, Ronald M.

```

; APPLICANT: Shukla, Rajiv
; TITLE OF INVENTION: IMMUNOGLOBULIN CONSTRUCT CONTAINING ANTI-MUCIN VARIABLE DOMAIN SE
; TITLE OF INVENTION: FOR ELICITING AN ANTI-IDIOTYPE ANTI-TUMOR RESPONSE
; FILE REFERENCE: 02755/100273-US1
; CURRENT APPLICATION NUMBER: US/10/469,125
; CURRENT FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: US 60/281,182
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/US02/10304
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-469-125-8

Query Match      71.4%; Score 40; DB 16; Length 126;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 QYSKLPWT 9
Db      109 QYNSLPWT 116

RESULT 24
; US-09-187-693-62
; Sequence 62, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(153)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-187-693-62

Query Match      71.4%; Score 40; DB 9; Length 153;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 HOYSKLPWT 9
Db      91 HOYSTPWT 99

RESULT 25
; US-09-187-693-66
; Sequence 66, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
```

```

; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 159
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(159)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-187-693-66

Query Match      71.4%; Score 40; DB 9; Length 159;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 HOYSKLPWT 9
Db      88 HOYSTPWT 96

RESULT 26
; US-09-056-160B-6
; Sequence 6, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Haasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
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TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-6

Query Match
Best Local Similarity 69.6%; Score 39; DB 9; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXSKLPWT 9
DB 2 QXSVPMWT 9

RESULT 27

US-09-217-268B-31
Sequence 31, Application US/09217268B
Patent No. US20020065398A1
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriguez, Rolando P
APPLICANT: Frias, Ernesto M
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
FILE REFERENCE: 2720.1US
CURRENT APPLICATION NUMBER: US/09/217,268B
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Murine
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-31

Query Match
Best Local Similarity 69.6%; Score 39; DB 9; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXSKLPWT 9
DB 2 QXSVPMWT 9

RESULT 28

US-10-234-671-6
Sequence 6, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wellis, James A.
Prestia, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94060
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinpatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-234-671-6

QY 2 QXSKLPWT 9
DB 2 QXSVPMWT 9

Query Match
Best Local Similarity 69.6%; Score 39; DB 14; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 29

US-10-624-153-25
Sequence 25, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MILLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 25
LENGTH: 9
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-9
OTHER INFORMATION: variant CDR sequence
US-10-624-153-25

Query Match
Best Local Similarity 69.6%; Score 39; DB 15; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXSKLPWT 9
DB 2 QXSVPMWT 9

RESULT 30
US-10-425-115-293070
Sequence 293070, Application US/10425115

```
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21 (53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 293070
/ LENGTH: 64
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_30360C.1.pep
US-10-425-115-293070
```

```
Query Match          69.6%; Score 39; DB 17; Length 64;
Best Local Similarity 55.6%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 QYSKIPWT 9
DB 51 HRYRRAPWT 59
```

```
RESULT 31
US-10-379-392-100
/ Sequence 100, Application US/10379392
/ Publication No. US20040110226A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazar, Gregory Alan
/ APPLICANT: Marshall, John Rudolf
/ APPLICANT: Dahljat, Basail I.
/ TITLE OF INVENTION: ANTIBODY OPTIMIZATION
/ FILE REFERENCE: A-71386-3 463077-236
/ CURRENT APPLICATION NUMBER: US/10/379,392
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/360,843
/ PRIOR FILING DATE: 2002-03-01
/ PRIOR APPLICATION NUMBER: US 60/384,197
/ PRIOR FILING DATE: 2002-05-29
/ NUMBER OF SEQ ID NOS: 184
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 100
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Humanized
US-10-379-392-100
```

```
Query Match          69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 QYSKIPWT 9
DB 90 QYSTVPWT 97
```

```
RESULT 32
US-10-379-392-121
/ Sequence 121, Application US/10379392
/ Publication No. US20040110226A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazar, Gregory Alan
/ APPLICANT: Desjarlais, John Rudolf
/ APPLICANT: Marshall, Shannon Alicia
```

```
/ APPLICANT: Dahljat, Basail I.
/ TITLE OF INVENTION: ANTIBODY OPTIMIZATION
/ FILE REFERENCE: A-71386-3 463077-236
/ CURRENT APPLICATION NUMBER: US/10/379,392
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/360,843
/ PRIOR FILING DATE: 2002-03-01
/ PRIOR APPLICATION NUMBER: US 60/384,197
/ PRIOR FILING DATE: 2002-05-29
/ NUMBER OF SEQ ID NOS: 184
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 121
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-379-392-121
```

```
Query Match          69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 QYSKIPWT 9
DB 90 QYSTVPWT 97
```

```
RESULT 33
US-10-379-392-123
/ Sequence 123, Application US/10379392
/ Publication No. US20040110226A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazar, Gregory Alan
/ APPLICANT: Marshall, John Rudolf
/ APPLICANT: Dahljat, Basail I.
/ TITLE OF INVENTION: ANTIBODY OPTIMIZATION
/ FILE REFERENCE: A-71386-3 463077-236
/ CURRENT APPLICATION NUMBER: US/10/379,392
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/360,843
/ PRIOR FILING DATE: 2002-03-01
/ PRIOR APPLICATION NUMBER: US 60/384,197
/ PRIOR FILING DATE: 2002-05-29
/ NUMBER OF SEQ ID NOS: 184
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 123
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-379-392-123
```

```
Query Match          69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 QYSKIPWT 9
DB 90 QYSTVPWT 97
```

```
RESULT 34
US-10-379-392-129
/ Sequence 129, Application US/10379392
/ Publication No. US20040110226A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazar, Gregory Alan
/ APPLICANT: Desjarlais, John Rudolf
/ APPLICANT: Marshall, Shannon Alicia
/ APPLICANT: Dahljat, Basail I.
```


TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT FILING DATE: 2003-03-03
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/384,197
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 129
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
NAME/KEY: MISC_FEATURE
LOCATION: (36)..(36)
OTHER INFORMATION: Xaa at position 36 can be Tyr, Phe, Met or Leu
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (43)..(43)
OTHER INFORMATION: Xaa at position 43 can be Tyr, Phe, His, Asp, Thr, Ala, Asn or
OTHER INFORMATION: Ser
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (87)..(87)
OTHER INFORMATION: Xaa at position 87 can be Phe, Tyr or Met
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (89)..(89)
OTHER INFORMATION: Xaa at position 89 can be Met or Gln
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (98)..(98)
OTHER INFORMATION: Xaa at position 98 can be Phe or Tyr
US-10-379-392-129

Query Match 69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLPMT 9
Db 90 QYSTVPM 97

RESULT 35
US-10-379-392-131
Sequence 131, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjardais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basail I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 131
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic

US-10-379-392-131
Query Match 69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLPMT 9
Db 90 QYSTVPM 97

RESULT 36
US-09-056-160B-13
Sequence 13, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-13

Query Match 69.6%; Score 39; DB 9; Length 107;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLPMT 9
Db 90 QYSTVPM 97

RESULT 37
US-09-056-160B-15
Sequence 15, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.

APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet B.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-15

Query Match 69.6%; Score 39; DB 9; Length 107;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QVSKLPMT 9
Db 90 QYSTVPMT 97

RESULT 38
US-10-234-671-13
Sequence 13, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-10-234-671-13

Query Match 69.6%; Score 39; DB 14; Length 107;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QVSKLPMT 9
Db 90 QYSTVPMT 97

RESULT 39
US-10-234-671-15
Sequence 15, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-234-671-15

Query Match 69.6%; Score 39; DB 14; Length 107;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSKLPWT 9
|||:||||
Db 90 QYSTVPWT 97

RESULT 40
US-10-251-215-49
; Sequence 49, Application US/10251215
; Publication No. US20030219839A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Fredrickson, Shana
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED
; FILE REFERENCE: 1087-36
; CURRENT APPLICATION NUMBER: US/10/251,215
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,537
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/323,544
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/379,980
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 107
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized Light Chain
US-10-251-215-49

Query Match 69.6%; Score 39; DB 14; Length 107;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSKLPWT 9
|||:||||
Db 89 QRSKLPWT 96

Search completed: December 17, 2004, 18:38:02
Job time : 18.3933 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:11:22 ; Search time 3.53933 Seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQSKLPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	85.7	111	2	G38740
2	48	85.7	111	2	E38740
3	45	80.4	111	2	A38740
4	45	80.4	111	2	C38740
5	42	75.0	128	2	A47159
6	42	75.0	141	2	A49134
7	39	69.6	108	1	KIHUME
8	39	69.6	258	2	AF2204
9	38	67.9	288	2	T36237
10	38	67.9	363	2	T39701
11	38	67.9	581	2	C39768
12	38	67.9	602	1	ACHU
13	38	67.9	603	2	S70849
14	38	67.9	1289	1	RMKRR3
15	37	66.1	108	1	KIHOUU
16	37	66.1	134	1	K4HUI7
17	37	66.1	136	2	A49137
18	37	66.1	190	2	T31291
19	37	66.1	402	2	S47329
20	37	66.1	585	2	T47364
21	37	66.1	821	2	H71475
22	37	66.1	823	2	C81739
23	37	66.1	1582	2	A56248
24	36	64.3	103	2	S18731
25	36	64.3	111	1	KVMS13
26	36	64.3	518	2	D96681
27	36	64.3	588	2	T26193
28	35	62.5	106	2	P10262
29	35	62.5	109	2	S26336

30	35	62.5	125	2	S40333	Ig kappa chain V-J
31	35	62.5	140	2	H69405	hypothetical prote
32	35	62.5	296	2	B87293	hydrolase, probabl
33	35	62.5	312	2	T27004	hypothetical prote
34	35	62.5	318	2	B83527	hypothetical prote
35	35	62.5	376	2	T46096	hypothetical prote
36	35	62.5	413	2	T18945	hypothetical prote
37	35	62.5	431	2	A89761	hypothetical prote
38	35	62.5	440	2	T44138	hypothetical prote
39	35	62.5	492	2	T18221	chromosome condens
40	35	62.5	535	2	JC5762	cytokine-inducible
41	35	62.5	549	2	B83149	probable acyl-CoA
42	35	62.5	574	2	B23677	complement C9 prec
43	35	62.5	609	2	AE2062	gamma-glutamyltran
44	35	62.5	788	1	JDVJLH	DNA-directed DNA p
45	35	62.5	1102	2	S28104	probable DNA-direc

ALIGNMENTS

RESULT 1

G38740
Ig kappa chain V region (Py54) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C/Accession: G38740
R./Ref: Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A./Title: Heavy and light chain variable region sequences and antibody properties of anti-
A./Reference number: A38740; PMID:9117923; PMID:1706720
A./Accession: G38740
A./Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A./Molecule type: mRNA
A./Residues: 1-111 <RUF>
A./Cross-references: UNIPROT:Q91WS9
C./Superfamily: immunoglobulin V region; immunoglobulin homology
C./Keywords: heterotetramer; immunoglobulin
F./19-93/Domain: immunoglobulin homology <IMW>

Query Match

Best Local Similarity 85.7%; Score 48; DB 2; Length 111;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 93 QYSKLPWT 100

RESULT 2

E38740
Ig kappa chain V region (Py54) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C/Accession: E38740
R./Ref: Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A./Title: Heavy and light chain variable region sequences and antibody properties of anti-
A./Reference number: A38740; PMID:9117923; PMID:1706720
A./Accession: E38740
A./Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A./Molecule type: mRNA
A./Residues: 1-111 <RUF>
A./Cross-references: UNIPROT:Q91WS9
C./Superfamily: immunoglobulin V region; immunoglobulin homology
C./Keywords: heterotetramer; immunoglobulin
F./19-93/Domain: immunoglobulin homology <IMW>

Query Match

Best Local Similarity 85.7%; Score 48; DB 2; Length 111;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

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Db      93 QYSKLPWT 100
|||||
RESULT 3
A38740
Ig kappa chain V region (Py20) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: A38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A>Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: A38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 111;
Best Local Similarity 87.5%; Pred. No. 0.44;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
|||||
Db      93 QYSKVPWT 100

RESULT 4
C38740
Ig kappa chain V region (Py2) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: C38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A>Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: C38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 111;
Best Local Similarity 87.5%; Pred. No. 0.44;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
|||||
Db      93 QYSKVPWT 100

RESULT 5
A47159
Ig lambda chain V region (CEA-specific maid T84.66) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A47159
R:Gaida, F.U.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumater, M.
J. Biol. Chem. 268, 14138-14145, 1993
A>Title: Molecular characterization of a cloned idiotypic cascade containing a network a
A:Reference number: A47159; MUID:93300804; PMID:7686150
A:Accession: A47159
A:Status: preliminary
A:Molecule type: DNA; protein
```

```
A:Residues: 1-128 <GAT>
A:Experimental source: hybridoma 6G6.C4
A>Note: sequence extracted from NCBI backbone (NCBIN:134419, NCBIPI:134420)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match      75.0%; Score 42; DB 2; Length 128;
Best Local Similarity 66.7%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
|||||
Db      109 HOYDNVPWT 117

RESULT 6
A49134
Ig kappa chain V-I region (ISE) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49134; S25115
R:Rocca, A.; Khamilchi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L.
Clin. Exp. Immunol. 91, 506-509, 1993
A>Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light
A:Reference number: A49134; MUID:93185310; PMID:7680298
A:Accession: A49134
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-141 <ROC>
A:Cross-references: EMBL:X67322; NID:g33268; PIDN:CA47736.1; PID:g33269
A>Note: sequence extracted from NCBI backbone (NCBIPI:127088)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match      75.0%; Score 42; DB 2; Length 141;
Best Local Similarity 66.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
|||||
Db      111 HOYDSVPWT 119

RESULT 7
K1HWME
Ig kappa chain V-I region (WEA) - human
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A01876
R:Goni, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A>Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) wit
A:Reference number: A93964; MUID:83273707; PMID:6410398
A:Accession: A01876
A:Molecule type: protein
A:Residues: 1-108 <GON>
A:Cross-references: UNIPROT:P01610
C:Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated ga)
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer
F:23-88/Disulfide bonds: #status predicted

Query Match      69.6%; Score 39; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 5.1;
```

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 QYSKLPWT 9
|||
90 QYSSFPWT 97

RESULT 8
AF2204
beta-carotene ketolase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2204
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchika, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; NCBI:21595285; PMID:11759840
A:Accession: AF2204
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:Q9Y8F0; GB:BA000019; PDB:BAE74888.1; PDB:1TJ32284; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alx3189
C:Superfamily: beta-carotene ketolase

Query Match 69.6%; Score 39; DB 2; Length 258;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
||:|:|
DB 240 HEYQDLPW 247

RESULT 9
T36237
probable phosphotransferase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T36237
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21577
A:Accession: T36237
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-288 <OLI>
A:Cross-references: UNIPROT:Q9X8F0; EMBL:AL049573; PDB:1CAB40335.1; GSPDB:GN00070; SCOP:
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOPDB:SCB39.27C

Query Match 67.9%; Score 38; DB 2; Length 288;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
||:|:|
DB 256 HVSQDLPW 263

RESULT 10
T39701
lipase-protein lipase A - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39701
R:Wood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrett, B.G.
submitted to the EMBL Data Library, July 1999

A:Reference number: Z21870
A:Accession: T39701
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-363 <WOO>
A:Cross-references: UNIPROT:Q13629; EMBL:AL109652; PDB:1CAB51768.1; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid C17A3
C:Genetics:
A:Gene: p1038
A:Map position: 2

Query Match 67.9%; Score 38; DB 2; Length 363;
Best Local Similarity 55.6%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 9
||:|:|
DB 322 HBUSLPWT 330

RESULT 11
C39768
cholinesterase (EC 3.1.1.8) - rabbit
N:Alternate names: butyrylcholinesterase
C:Species: Oryzctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S10255; C39768
R:Jbilo, O.; Chatonnet, A.
Nucleic Acids Res. 18, 3990, 1990
A:Title: Complete sequence of rabbit butyrylcholinesterase.
A:Reference number: S10255; NCBI:90326526; PMID:2374720
A:Accession: S10255
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-581 <RBI>
A:Cross-references: UNIPROT:P21927; EMBL:X52090; NID:G1476; PDB:1CAA36308.1; PDB:1G17027;
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogr
J. Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A:Reference number: A39768; NCBI:91201348; PMID:2016308
A:Accession: C39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 75-215 <ARP>
A:Cross-references: GB:M62779; NID:G164788; PDB:1AAA1169.1; PDB:G164789
C:Genetics:
A:Insertions: 485/2; 541/1
A:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:35-535/Domain: cholinesterase homology <CHE>

Query Match 67.9%; Score 38; DB 2; Length 581;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
||:|:|
DB 430 HRSSKLPW 437

RESULT 12
ACHU
cholinesterase (EC 3.1.1.8) precursor [validated] - human
N:Alternate names: acetylcholine acetylhydrolase; butyrylcholinesterase; choline esterase II;
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: A33769; A26613; A33887; A34668; A00772
R:Arpagaus, M.; Kott, M.; Vacaris, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
Biochemistry 29, 124-131, 1990
A:Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single co
A:Reference number: A33769; NCBI:90212557; PMID:2322535
A:Accession: A33769
A:Molecule type: DNA

A:Residues: 'MSVQSNLQAGAAAACISPKYVWIFTPCKLCHLCRESEIN',1-602 <ARP>
A:Cross-references: UNIPROT:P06276; GB:M32391; GB:J02879
A>Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra
R:Prody, C.A.; Zevin-Soukin, D.; Gnatt, A.; Goldberg, O.; Soreq, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987
A:Title: Isolation and characterization of full-length cDNA clones coding for cholinesterase
A:Reference number: A26613; MUID:87231856; PMID:3035356
A:Accession: A26613
A:Molecule type: mRNA
A:Residues: 1-133,'D',135-602 <PRO>
R:McTernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A:Title: Brain cDNA clone for human cholinesterase.
A:Reference number: A33887; MUID:88016155; PMID:3477799
A:Accession: A33887
A:Molecule type: mRNA
A:Residues: 'MSVQSNLQAGAAAACISPKYVWIFTPCKLCHLCRESEIN',1-602 <MCT>
A>Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra
R:Moguelita, C.F.; McGuire, W.C.; Graesser, C.; Bartels, C.F.; Arpagaus, W.; Van der Spek,
Am. J. Hum. Genet. 46, 934-942, 1990
A:Title: Identification of a frameshift mutation responsible for the silent phenotype of
A:Reference number: A34668; MUID:90252779; PMID:2339692
A:Accession: A34668
A:Molecule type: DNA
A:Residues: 143-145,'VSNNMIIPTCL',<NOG>
A>Note: frameshift mutant in codon for residue 145 (Gly)
R:Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.
J. Biol. Chem. 262, 549-557, 1987
A:Title: Complete amino acid sequence of human serum cholinesterase.
A:Reference number: A00772; MUID:87109144; PMID:3542989
A:Accession: A00772
A:Molecule type: protein
A:Residues: 29-602 <LOC>
A:Experimental source: Plasma
C:Comment: Cholinesterase is present in most cells (except erythrocytes).
C:Genetics: GDB:BCHR; CHE1
A:Gene: GDB:BCHR; CHE1
A:Cross-references: GDB:120558; OMIM:177400
A:Map position: 3q26.1-3q26.2
A:introns: 506/2; 562/1
C:Function:
A:Description: hydrolyses acylcholines to choline and a carboxylic acid
A>Note: this cholinesterase is highly reactive with organophosphate esters
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F:1-28/Domain: signal sequence #status predicted <Sig>
F:29-602/Product: cholinesterase #status experimental <Mat>
F:56-556/Domain: cholinesterase homology <CHR>
F:45,85,134,269,284,369,483,509,514/Binding site: carbohydrate (Asn) (covalent) #status
F:226/Active site: Ser #status experimental

Query Match 67.9%; Score 38; DB 1; Length 602;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
Db 451 HRSSKLPW 458

RESULT 13
S70849
cholinesterase (EC 3.1.1.8) - mouse
N:Alternate names: butyrylcholine esterase
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence revision 08-Nov-1996 #text_change 09-Jul-2004
C:Accession: S70849; S15680; A39768
R:Taylor, P.
submitted to the EMBL Data Library, August 1992
A:Reference number: S70849
A:Accession: S70849
A:Molecule type: nucleic acid
A:Residues: 1-603 <TAY>

A:Cross-references: UNIPROT:Q03311; EMBL:M99492; NID:g191579; PID:AA37328.1; PID:g19157
R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternat
A:Reference number: JH0314; MUID:90380429; PMID:2400605
A:Accession: S15680
A:Status: nucleic acid sequence not shown
A:Molecule type: nucleic acid
A:Residues: 30-128,'P',130-603 <RAC>
A:Cross-references: EMBL:M99492
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
J. Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A:Reference number: A39768; MUID:91201348; PMID:2016308
A:Accession: A39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 97-128,'P',130-237 <ARP>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:57-557/Domain: cholinesterase homology <CHE>

Query Match 67.9%; Score 38; DB 2; Length 603;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
Db 452 HRSSKLPW 459

RESULT 14
RXNR3
mRNA guanylyltransferase (EC 2.7.7.50) - reovirus type 3
N:Alternate names: lambda 2 protein; mRNA capping enzyme
C:Species: reovirus type 3 (man)
A>Note: host Homo sapiens (man)
C>Date: 30-Sep-1989 #sequence revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A28471
R:Seiliger, L.S.; Zheng, K.; Shatkin, A.J.
J. Biol. Chem. 262, 16289-16293, 1987
A:Title: Complete nucleotide sequence of reovirus L2 gene and deduced amino acid sequence
A:Reference number: A28471; MUID:88058999; PMID:2824487
A:Accession: A28471
A:Molecule type: DNA
A:Residues: 1-1289 <SEL>
A:Cross-references: UNIPROT:P11079
C:Genetics:
A:Map position: segment L2
C:Superfamily: reovirus mRNA guanylyltransferase
C:Keywords: core protein; mRNA capping; nucleotidyltransferase; transcription

Query Match 67.9%; Score 38; DB 1; Length 1289;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 9
Db 659 HQHSLTWT 667

RESULT 15
KIHUAV
Ig kappa chain V-I region (Au) - human
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence revision 02-Jul-1998 #text_change 09-Jul-2004
C:Accession: A91653; A01862; S02573
R:Schlecht, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Subg
A:Reference number: A91653; MUID:72189444; PMID:5028201
A:Accession: A91653
A:Molecule type: protein

A:Residues: 1-108 <SCH>
 A:Cross-references: UNIPROT:P01594
 A>Note: the C region of this chain has the Inv (3) marker
 R:Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Strel
 Biophys. Struct. Mech. 1, 139-146, 1975
 A>Title: The structure determination of the variable portion of the Bence-Jones protein
 A:Reference number: A90729; PMID:77022433; PMID:1234024
 A:Contents: annotation; X-ray crystallography
 A>Note: the structure of the V region was determined by molecular replacement methods us
 R:Steiner, V.; Chang, J.Y.
 FEBS Lett. 222, 6-10, 1987
 A>Title: Chemical modification of the carboxyl groups of protein substrates enhances the
 A:Reference number: S0572; PMID:88005152; PMID:3115831
 A:Contents: annotation
 A:Comment: This is a Bence Jones protein.
 C:Genetics:
 A:Gene: GDB:1GKVI
 A:Cross-references: GDB:136264
 A:Map position: 2p12-2p12
 C:Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kap
 hain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:23-88/Disulfide bonds: #status predicted

Query Match 66.1%; Score 37; DB 1; Length 108;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
 DB 90 QYDLPWT 97

RESULT 16

K4HU17
 Ig kappa chain precursor V-IV region (BI7) - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
 C:Accession: A01905
 R:Marsh, P.; Miller, F.; Gould, H.
 Nucleic Acids Res. 13, 6531-6544, 1985
 A>Title: Detection of a unique human VkapaiV germline gene by a cloned cDNA probe.
 A:Reference number: A01905; PMID:86041854; PMID:2997713
 A:Accession: A01905
 A:Molecule type: mRNA
 A:Residues: 1-134 <MAR>
 A>Note: the sequence was determined from the differentiated gene
 A>Note: the authors translated the codon TGC for residue 76 as Trp
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-134/Product: Ig kappa chain V-IV region (BI7) #status predicted <MAR>
 F:21-43/Region: framework 1
 F:36-116/Domain: immunoglobulin homology <IMM>
 F:44-60/Region: complementarity-determining 1
 F:61-75/Region: framework 2
 F:76-82/Region: complementarity-determining 2
 F:83-114/Region: framework 3
 F:115-121/Region: complementarity-determining 3
 F:122-134/Region: framework 4
 F:43-114/Disulfide bonds: #status predicted

Query Match 66.1%; Score 37; DB 1; Length 134;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
 DB 116 QYDLPWT 123

RESULT 17

A49137
 Ig kappa chain precursor V region - human
 C:Species: Homo sapiens (man)
 C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A49137; S24479
 R:Khamlichi, A.A.; Aucuttier, P.; Silvain, C.; Bauwens, M.; Touchard, G.; Freud'homme,
 Clin. Exp. Immunol. 87, 122-126, 1992
 A>Title: Primary structure of a monoclonal kappa chain in myeloma with light chain depos
 A:Reference number: A49137; PMID:92127887; PMID:1733627
 A:Accession: A49137
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-136 <KHA>
 A:Cross-references: GB:X64135; GB:S79324; NID:G33059; PIDN:CAA45496.1; PID:G33060
 A>Note: sequence extracted from NCBI backbone (NCBIN:79324, NCBI:P:79325)
 R:Cogne, M.C.C.
 submitted to the EMBL Data Library, January 1992
 A:Reference number: S24479
 A:Accession: S24479
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-136 <COG>
 A:Cross-references: EMBL:X64135; NID:G33059; PIDN:CAA45496.1; PID:G33060
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 66.1%; Score 37; DB 2; Length 136;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
 DB 116 QYDLPWT 123

RESULT 18

TJ1291
 hypothetical protein 1251 - Sphingomonas aromaticivorans plasmid pNL1
 C:Species: Sphingomonas aromaticivorans
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: TJ1291
 R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Stok, E.C.; Sensen, C.W.; Ge
 submitted to the EMBL Data Library, July 1998
 A:Description: Complete sequence of a 184 Kb catabolic plasmid from Sphingomonas aromatic
 A:Reference number: Z20992
 A:Accession: TJ1291
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-190 <ROM>
 A:Cross-references: UNIPROT:O85999; EMBL:AF079317; NID:G3378261; PID:G3378432; PIDN:AD00
 C:Genetics:
 A:Genome: plasmid pNL1
 A>Note: orf1251

Query Match 66.1%; Score 37; DB 2; Length 190;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSLPWT 8
 DB 114 HOYRLRW 121

RESULT 19

S47329
 OXAL protein precursor - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: PBT1402 protein; protein YER134W
 C:Species: Saccharomyces cerevisiae
 C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004

C/Accession: S47329, S50657, S46384, A36328, S51575, S12291
R.Pratlje, E.
submitted to the EMBL Data Library, August 1993
A/Reference number: S47329
A/Accession: S47329
A/Molecule type: DNA
A/Residues: 1-402 <PRA>
A/Cross-references: UNIPROT:P39952; EMBL:X74456; NID:g521091; PID:g521092
R.Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A/Description: The sequence of *S. cerevisiae* cosmid 8229, 9115, 9132, 9981, and lambda
A/Reference number: S50657
A/Accession: S50657
A/Molecule type: DNA
A/Residues: 1-402 <DIE>
A/Cross-references: EMBL:U18917; NID:g603394; MIPS:YER154W
R.Bonney, N.; Chaiwet, F.; Hamel, P.; Slonimski, P.P.; Dujardin, G.
J. Mol. Biol. 239, 201-212, 1994
A/Title: OXA1, a Saccharomyces cerevisiae nuclear gene whose sequence is conserved from
A/Reference number: S46384; M0ID:94254098; PMID:8196054
A/Accession: S46384
A/Molecule type: DNA
A/Residues: 1-107, 'R', 109-402 <BON>
A/Cross-references: EMBL:X77558
R.Ohmen, J.D.; Burke, K.A.; McEwen, J.E.
Mol. Cell. Biol. 10, 3027-3035, 1990
A/Title: Divergent overlapping transcripts at the PET122 locus in *Saccharomyces cerevisiae*
A/Reference number: A36328; M0ID:90258894; PMID:2160592
A/Accession: A36328
A/Molecule type: DNA
A/Residues: 1-379 <OHM>
A/Cross-references: GB:X07558
R.Bauer, M.; Behrens, M.; Esser, K.; Michaelis, G.; Pratlje, E.
Mol. Gen. Genet. 245, 272-278, 1994
A/Title: PET1402, a nuclear gene required for proteolytic processing of cytochrome oxidase
A/Reference number: S51575; M0ID:95115677; PMID:7816036
A/Accession: S51575
A/Molecule type: DNA
A/Residues: 1-402 <BAU>
A/Cross-references: EMBL:X74456; NID:g521091; PIDN:CAA52465.1; PID:g521092
C/Genetics:
A/Gene: SGD:OXA1; PET1402
A/Cross-references: SGD:S0000956; MIPS:YER154W
A/Map position: 5R
A/Genome: nuclear
C/Function:
A/Description: required for a post-translational step in cytochrome oxidase biogenesis
A/Keywords: mitochondrion; transmembrane protein
F:108-316/Domain: stage III sporulation protein homology <SPOR>

Query Match 66.1%; Score 37; DB 2; Length 402;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 121 HVSGLPW 128

RESULT 20
T47364
Hypothetical protein F7M19.70 - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: T47364
R.Nyakatura, G.; Fattmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24458
A/Accession: T47364
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-585 <NYA>

A/Cross-references: UNIPROT:Q9M255; EMBL:AL136643
A/Experimental source: Cultivar Columbia; BAC clone F7M19
C/Genetics:
A/Map position: 3
A/Introns: 101/3; 233/2; 328/3; 361/2
A/Note: F7M19.70

Query Match 66.1%; Score 37; DB 2; Length 585;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 OYSKLPWT 9
DB 568 OYKPEWT 575

RESULT 21
H71475
probable chlr phosphoprotein - *Chlamydia trachomatis* (serotype D, strain UW3/Cx)
C/Species: *Chlamydia trachomatis*
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C/Accession: H71475
R.Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A/Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia tract*
A/Reference number: A71570; M0ID:9900809; PMID:9784136
A/Accession: H71475
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-821 <ARN>
A/Cross-references: UNIPROT:O84749; GB:AE001346; GB:AE001273; NID:g3329203; PIDN:AAC6833;
A/Experimental source: serotype D, strain UW-3/Cx
C/Genetics:
A/Gene: CT744

Query Match 66.1%; Score 37; DB 2; Length 821;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 273 HALSKLPW 280

RESULT 22
C81739
conserved hypothetical protein TC0120 [imported] - *Chlamydia muridarum* (strain Nigg)
C/Species: *Chlamydia muridarum*, *Chlamydia trachomatis* M0bn
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: C81739
R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, I.
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of *Chlamydia trachomatis* M0bn and *Chlamydia pneumoniae* AR39.
A/Reference number: AB1500; M0ID:20150255; PMID:10684935
A/Accession: C81739
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-823 <RET>
A/Cross-references: UNIPROT:Q9PL10; GB:AE002279; GB:AE002160; NID:g7190148; PIDN:AAF3899E
A/Experimental source: strain Nigg (M0bn)
C/Genetics:
A/Gene: TC0120

Query Match 66.1%; Score 37; DB 2; Length 823;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 272 HALSKLPW 279

RESULT 23

A56248
sulfonilylurea receptor - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 02-Feb-2001
C/Accession: A56248
R/Aguiar-Bryan, L.; Nichols, C.G.; Wechsler, S.W.; Clement IV, J.P.; Boyd III, A.E.; Gd
Science 268, 423-426, 1995
A/Title: Cloning of the beta cell high-affinity sulfonilylurea receptor: a regulator of in
A/Reference number: A56248; NCBI:5523252; PMID:7716547
A/Accession: A56248
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1582 <AGU>
A/Cross-references: GB:L40623
C/Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C/Keywords: ATP; glycoprotein; nucleotide binding; P-loop
F/2-1582/Product: sulfonilylurea receptor #status experimental <MAT>
F/696-906/Domain: ATP-binding cassette homology <ABC1>
F/713-720/Region: nucleotide-binding motif A (P-loop)
F/1362-1555/Domain: ATP-binding homology <ABC2>
F/1378-1386/Region: nucleotide-binding motif A (P-loop)
F/10/Binding site: cardonhydrate (Asn) (covalent) #status experimental

Query Match 66.1%; Score 37; DB 2; Length 1582;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 8
DB 991 HOYAKIPW 998

RESULT 24

S18731
Ig kappa chain V-J region (MSI-N17) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 23-Jul-1999
C/Accession: S18731
R/Hiruma, T.; Takehita, S.; Yoshida, Y.; Yamagishi, H.
ImmunoL. Lett. 27, 19-24, 1991
A/Title: Structure of extrachromosomal circular DNAs generated by immunoglobulin light c
A/Reference number: S18731; NCBI:91209891; PMID:1502191
A/Accession: S18731
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-103 <HIR>
A/Cross-references: EMBL:X54753; NID:G55294; PIDN:CA38555.1; PID:G55295
A/Experimental source: spleen, strain BALB/c-nu/nu
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1990
C/Complex: An immunoglobulin heterodimer subunit consists of two identical light (leg
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterodimer; immunoglobulin
F/11-85/Domain: immunoglobulin homology <IMM>
F/18-83/Disulfide bonds: #status predicted

Query Match 64.3%; Score 36; DB 2; Length 103;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 OYSKLPWT 9
DB 85 OHSYLPWT 92

RESULT 25

KVMS13
Ig kappa chain V region (PC2413) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C/Accession: A01932
R/Welger, M.; Galtman, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978
A/Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A/Reference number: A93204; NCBI:79073152; PMID:103003
A/Accession: A01932
A/Molecule type: protein
A/Residues: 1-111 <WEI>

A/Cross-references: UNIPROT:P01657
C/Complex: An immunoglobulin heterodimer subunit consists of two identical light (kappa
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterodimer
F/16-94/Domain: immunoglobulin homology <IMM>
F/23-92/Disulfide bonds: #status predicted

Query Match 64.3%; Score 36; DB 1; Length 111;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
DB 93 HOYKVPWT 101

RESULT 26

D96681
Protein F1E22.2 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D96681
R/Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; NCBI:2106719; PMID:11130712
A/Accession: D96681
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-518 <STO>
A/Cross-references: UNIPROT:Q9SH20; GB:AB005173; NID:G666412; PIDN:AAF23846.1; GSPDB:GN0

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-518 <STO>
A/Cross-references: UNIPROT:Q9SH20; GB:AB005173; NID:G666412; PIDN:AAF23846.1; GSPDB:GN0
A/Map position: 1
C/Superfamily: Escherichia coli trypsin-like proteinase degs; GIGF domain homology; tryp

Query Match 64.3%; Score 36; DB 2; Length 518;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 7
DB 387 HOYDKLP 393

RESULT 27

T26193
hypothetical protein W05E10.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26193
R/Mortimore, B.
submitted to the EMBL Data Library, July 1996
A/Reference number: Z20168
A/Accession: T26193
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-588 <WIL>
A/Cross-references: UNIPROT:Q23176; EMBL:Z77670; PIDN:CA801250.1; GSPDB:GN00023; CESP:W01

A:Experimental source: clone W05E10
C:Gene: CESP:W05E10.4
A:Map position: 5
A:Introns: 25/3; 37/2; 71/1; 103/2; 133/1; 299/3; 329/3; 428/3; 479/3; 504/3; 523/3
C:Superfamily: human alpha,alpha-trehalase

Query Match 64.3%; Score 36; DB 2; Length 588;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXSKLPWT 8
DB 568 KYAKLPW 574

RESULT 28
PL0262
Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0262
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Plisetaky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A:Reference number: PL0231; PMID:90111618; PMID:2104919
A:Accession: PL0262
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 62.5%; Score 35; DB 2; Length 106;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXSKLPWT 9
DB 90 QXASYPWT 97

RESULT 29
S26336
Ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26336
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein A:Reference number: S26309; PMID:91341421; PMID:1908510
A:Accession: S26336
A:Molecule type: mRNA
A:Residues: 1-109 <STA>
A:Cross-references: EMBL:X59201
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-95/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 35; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOXSKLPWT 9
DB 111

DB 94 HQHSTPWT 102

RESULT 30
S40333
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; PMID:94080891; PMID:8258341
A:Accession: S40333
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <RTB>
A:Cross-references: EMBL:X72443; NID:G441354; PIDN:CAA5111.1; PID:G441355
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 35; DB 2; Length 125;
Best Local Similarity 62.5%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXSKLPWT 9
DB 108 QXNSYPWT 115

RESULT 31
H69405
hypothetical protein AF1249 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H69405
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Urtreback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.J.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo A:Reference number: A69250; PMID:98049343; PMID:9389475
A:Accession: H69405
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-140 <RTB>
A:Cross-references: UNIPROT:Q29019; GB:AE001018; GB:AE000782; NID:G2689341; PIDN:AA9000;
C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF1249

Query Match 62.5%; Score 35; DB 2; Length 140;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOXSKLPWT 9
DB 36 HNGIKLPWT 44

RESULT 32
B87293
hydroxylase, probable [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 12-Jul-2004
C:Accession: B87293
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonite n, J.; Ermolova, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete genome sequence of Caulobacter crescentus.
A:Reference number: AB7249; PMID:21173698; PMID:11259647

A/Accession: B87293
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-296 <STO>
A/Cross-references: UNIPROT:Q9AB76; GB:AE005673; NID:g13421508; PIDN:AAK2342.1; GSPDB:CC0355
C/Genetics:
C/Superfamily: tropinesterase

Query Match 62.5%; Score 35; DB 2; Length 296;
Best Local Similarity 71.4%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSKLPW 9
Db 144 YAKAPW 150

RESULT 33

T27004

hypothetical protein Y48B6A.14 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T27004

A/Reference number: Z20297

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-312 <MIL>

A/Cross-references: UNIPROT:Q9U2A0; EMBL:AL110490; NID:e1542263; PIDN:CAB54448.1; CESP:Y

A/Experimental source: clone Y48B6A

C/Genetics:

A/Gene: CESP:Y48B6A.14

A/Introns: 132/1; 210/1; 288/3

Query Match 62.5%; Score 35; DB 2; Length 312;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YSKLPW 8
Db 19 YSKLPW 24

RESULT 34

B83527

hypothetical protein PA0955 [imported] - *Pseudomonas aeruginosa* (strain PA01)C/Species: *Pseudomonas aeruginosa*

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: B83527

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-318 <STO>

A/Cross-references: UNIPROT:Q91503; GB:AE004529; GB:AE004091; NID:g946851; PIDN:AA0434

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA0955

A/Introns: 132/1; 210/1; 288/3

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-318 <STO>

A/Cross-references: UNIPROT:Q91503; GB:AE004529; GB:AE004091; NID:g946851; PIDN:AA0434

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA0955

Query Match 62.5%; Score 35; DB 2; Length 318;
Best Local Similarity 71.4%; Pred. No. 84;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YSKLPW 8
Db 19 YSKLPW 24

Db 166 EYSSLPW 172

RESULT 35

T46096

hypothetical protein T25B15.30 - *Arabidopsis thaliana*C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C/Accession: T46096

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-376 <ALC>

A/Cross-references: UNIPROT:Q9FT56; EMBL:AL132972

A/Experimental source: cultivar Columbia; BAC clone T25B15

C/Genetics:

A/Map position: 3

A/Introns: 31/1; 51/2; 60/3; 76/2; 106/3; 163/1; 191/2; 226/3; 252/1; 274/3; 298/1; 326/1

A/Note: T25B15.30

Query Match 62.5%; Score 35; DB 2; Length 376;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YSKLPW 8
Db 83 YSKLPW 88

RESULT 36

T18945

hypothetical protein C05C10.4 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18945

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-413 <MIL>

A/Cross-references: UNIPROT:Q09451; EMBL:Z48178; PIDN:CA88205.1; GSPDB:GN00020; CESP:COE

A/Experimental source: clone C05C10

C/Genetics:

A/Gene: CESP:C05C10.4

A/Map position: 2

A/Introns: 31/3; 96/3; 128/1; 155/3; 185/3; 255/1; 313/3; 360/3; 407/3

C/Superfamily: mammalian acid phosphatase

Query Match 62.5%; Score 35; DB 2; Length 413;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YSKLPW 8
Db 225 YAKLPW 230

RESULT 37

A89761

hypothetical protein [imported] - *Staphylococcus aureus* (strain N315)C/Species: *Staphylococcus aureus*

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: A89761

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-376 <ALC>

A/Cross-references: UNIPROT:Q9FT56; EMBL:AL132972

A/Experimental source: cultivar Columbia; BAC clone T25B15

C/Genetics:

A/Map position: 3

A/Introns: 31/1; 51/2; 60/3; 76/2; 106/3; 163/1; 191/2; 226/3; 252/1; 274/3; 298/1; 326/1

A/Note: T25B15.30

A/Reference number: A89758; MUID:21311952; PMID:11418146
 A/Accession: A89761
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-431 <KUR>
 A/Cross-references: UNIPROT:Q9XB68; GB:BA000018; PID:G13699942; PIDN:BA841241.1; GSPDB:C
 A/Experimental source: strain N315
 C/Genetics:
 A/Note: SA0024

Query Match 62.5%; Score 35; DB 2; Length 431;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8
 |||:
 Db 77 YSKVPW 82

RESULT 38

T44138
 hypothetical protein [imported] - Staphylococcus aureus (fragment)

C/Species: Staphylococcus aureus

C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C/Accession: T44138

R/To, T.; Katayama, Y.; Hiramatsu, K.

Antimicrob. Agents Chemother. 43, 1449-1458, 1999

A/Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth

A/Reference number: Z22733; MUID:99278010; PMID:10348769

A/Accession: T44138

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-440 <ITO>

A/Cross-references: UNIPROT:Q9XB68; EMBL:D86934; PIDN:BA82240.1

A/Experimental source: strain N315

Query Match 62.5%; Score 35; DB 2; Length 440;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8
 |||:
 Db 86 YSKVPW 91

RESULT 39

T18221

chromosome condensation regulator protein - yeast (Candida albicans)

C/Species: Candida albicans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18221

R/Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, November 1998

A/Reference number: Z18831

A/Accession: T18221

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-492 <BAR>

A/Cross-references: UNIPROT:Q94013; EMBL:AL033396; PIDN:CAA21948.1

C/Genetics:

A/Note: Rc1-like

C/Superfamily: pheromone response pathway component SRM1

Query Match 62.5%; Score 35; DB 2; Length 492;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 7
 |||:
 Db 31 HSYSKLPW 37

RESULT 40

JCS762
 cytokine-inducible SH2 protein 4 - human
 C/Species: Homo sapiens (man)
 C/Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
 C/Accession: JCS762
 R/Masuhara, M.; Sakamoto, H.; Matsunoto, A.; Suzuki, R.; Yasukawa, H.; Mitsu, K.; Wakio
 Biochem. Biophys. Res. Commun. 239, 439-446, 1997
 A/Title: Cloning and characterization of novel CIS family genes.
 A/Reference number: JCS760; MUID:98008857; PMID:9344848
 A/Accession: JCS762
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-535 <MAS>

Query Match 62.5%; Score 35; DB 2; Length 535;
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
 |||:
 Db 130 HMYSPAPW 137

Search completed: December 17, 2004, 18:30:16
 Job time : 3.53933 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:29:23 ; Search time 26.8969 seconds
(without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-8
Perfect score: 56
Sequence: 1 HQYSKLPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniProt_sprot:*
2: uniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	78.6	107	2 Q9JL84	Q9JL84 mus musculi
2	43	76.8	770	2 Q9TOY1	Q9TOY1 lactobacilli
3	41	73.2	107	2 AAR11015	AAR11015 mus muscu
4	41	73.2	572	2 Q6BN22	Q6BN22 debaryomyce
5	40	71.4	623	2 Q8XVB0	Q8XVB0 ralsconia s
6	39	69.6	108	1 KVIR_HUMAN	P01610 homo sapien
7	39	69.6	258	2 Q8YSA0	Q8YSA0 anabaena sp
8	39	69.6	351	2 Q9VST8	Q9VST8 dirosophila
9	38	67.9	288	2 Q9XEP0	Q9XEP0 streptomyce
10	38	67.9	336	2 Q7NAA3	Q7NAA3 photorhabdu
11	38	67.9	349	2 Q9GKA6	Q9GKA6 sus scrofa
12	38	67.9	353	2 Q13629	Q13629 schizosacch
13	38	67.9	386	2 Q6FOG0	Q6FOG0 candida gla
14	38	67.9	389	2 Q89UG7	Q89UG7 bradyrhizob
15	38	67.9	434	2 Q7SB85	Q7SB85 aebhya goss
16	38	67.9	434	2 AAS1605	AAS1605 aebhya goss
17	38	67.9	581	1 CHLE_RABIT	P21927 oryctolagus
18	38	67.9	597	2 Q9JKC1	Q9JKC1 rattus norv
19	38	67.9	602	1 CHLE_HUMAN	P06276 homo sapien
20	38	67.9	603	1 CHLE_MOUSE	Q03311 mus musculi
21	38	67.9	603	2 Q90ZK8	Q90ZK8 gallus gall
22	38	67.9	603	2 BAC34196	BAC34196 mus muscu
23	38	67.9	657	2 Q6MT24	Q6MT24 bdellovibri
24	38	67.9	657	2 CAE78158	CAE78158 bdellovibri
25	38	67.9	658	2 Q8MY38	Q8MY38 papilio xuc
26	38	67.9	1036	2 Q6CJY8	Q6CJY8 kluyveromyc
27	38	67.9	1289	1 MCE_REOVD	P11079 reovirus ty
28	38	67.9	1289	2 Q91RA1	Q91RA1 reovirus ty
29	37	66.1	95	2 AAR11062	AAR11062 mus muscu
30	37	66.1	99	2 AAR11071	AAR11071 mus muscu
31	37	66.1	108	1 KVIB_HUMAN	P01594 homo sapien

32	37	66.1	108	2 Q9CTV5	Q9CTV5 mus musculi
33	37	66.1	134	1 KV4C_HUMAN	P06314 homo sapien
34	37	66.1	134	2 Q8VDD0	Q8VDD0 mus musculi
35	37	66.1	190	2 Q8S999	Q8S999 sphingomona
36	37	66.1	242	2 Q9PU09	Q9PU09 latimeria c
37	37	66.1	245	2 Q8UTT6	Q8UTT6 brachydanio
38	37	66.1	330	2 Q6MOC7	Q6MOC7 bdellovibri
39	37	66.1	330	2 CAE78520	CAE78520 bdellovibri
40	37	66.1	388	2 Q9PLA1	Q9PLA1 arabidopsis
41	37	66.1	402	1 OXAI_YEAST	P39952 saccharomyc
42	37	66.1	402	2 Q46434	Q46434 chlamydia t
43	37	66.1	444	2 Q56955	Q56955 human papil
44	37	66.1	566	2 Q7QFLI	Q7QFLI anopheles g
45	37	66.1	585	2 Q9M255	Q9M255 arabidopsis

ALIGNMENTS

RESULT 1					
ID	Q9JL84	PRELIMINARY;	PRT;	107 AA.	
AC	Q9JL84;				
DT	01-OCT-2000 (TREMBlrel. 15, Created)				
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	Anti-myosin immunoglobulin light chain variable region (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C;				
RX	MEDLINE=20448942; Pubmed=10992488;				
RA	Maikael S., Liao L., Cunningham M.W., Diamond B.;				
RT	"T-Cell-dependent antibody response to the dominant epitope of				
RT	streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive				
RT	with cardiac myosin."				
RL	Infect. Immun. 68:5803-5808(2000).				
DR	EMBL; AF206022; AAF69320.1; -.				
DR	HSSP; P01594; 1UV5.				
DR	Interpro; IPR007110; IG_1like.				
DR	Interpro; IPR003596; IG_V.				
DR	Pfam; PF00047; IG_1.				
DR	SMART; SM00406; IG_1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
FT	NON_TER 1				
FT	NON_TER 107				
FT	SEQUENCE 107 AA; 11648 MW; ACF9B1253ACAI8SD CRC64;				
Query Match					
Best Local Similarity 78.6%; Score 44; DB 2; Length 107;					
Matches 7; Conservativity 87.5%; Pred. No. 3.6;					
Matches 7; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	2 QYSKLPT 9				
Db	90 QYSKLPT 97				
RESULT 2					
ID	Q9TOY1	PRELIMINARY;	PRT;	770 AA.	
AC	Q9TOY1;				
DT	01-MAY-2000 (TREMBlrel. 13, Created)				
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DT	01-MAY-2004 (TREMBlrel. 26, Last annotation update)				
DE	Putative primase.				
OS	Lactobacillus casei bacteriophage A2.				
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.				
OX	NCBI_TaxID=51369;				
RN	[1]				

RP SEQUENCE FROM N.A.
RX MEDLINE=97197195; PubMed=9044284;
RA Garcia P., Alonso J.C., Suarez J.E.;
RT "Molecular Analysis of the cos Region of the Lactobacillus casei
RT Bacteriophage A2. Gene product 3, gp3, specifically binds to its
RT downstream cos region."; Mol. Microbiol. 23:505-514 (1997).
RN (12)
RP SEQUENCE FROM N.A.
RX MEDLINE=98317291; PubMed=9642205;
RA Ladero V., Garcia P., Baccaran V., Herrero M., Alvarez M.,
RA Suarez J.E.;
RT "Identification of the repressor-encoding gene of the Lactobacillus
RT bacteriophage A2."; J. Bacteriol. 180:3474-3476 (1998).
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE=98445458; PubMed=9770432;
RA Alvarez M.A., Herrero M., Suarez J.E.;
RT "The Site-Specific Recombination system of the Lactobacillus spp
RT Bacteriophage A2 integrates in Gram Positive and Gram Negative
RT Bacteria."; J. Virol. 250:185-193 (1998).
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE=20351728; PubMed=10891412;
RA Moscoso M., Suarez J.E.;
RT "Characterisation of the DNA replication module of bacteriophage A2
RT and use of its origin of replication as a defence against infection
RT during milk fermentation by Lactobacillus casei."; J. Virol. 273:101-111 (2000).
RN (5)
RP SEQUENCE FROM N.A.
RX MEDLINE=99214330; PubMed=10196287;
RA Garcia P., Ladero V., Alonso J.C., Suarez J.E.;
RT "Cooperative interaction of CI protein regulates lysogeny of
RT Lactobacillus casei by bacteriophage A2."; J. Virol. 73:3920-3929 (1999).
RN (6)
RP SEQUENCE FROM N.A.
RA Ladero V., Garcia P., Alonso J.C., Suarez J.E.;
RT "A2 Cro, the lysogenic cycle repressor, specifically binds to the
RT genetic switch region of Lactobacillus casei bacteriophage A2."; J. Virol. 262:222-229 (1999).
RN (7)
RP SEQUENCE FROM N.A.
RX MEDLINE=22262118; PubMed=12374837;
RA Proulx C., van Sinderen D., Suarez J., Garcia P., Ladero V.,
RA Fitzgerald G.F., Desiere F., Brunsow H.;
RT "The dilemma of phage taxonomy illustrated by comparative genomics of
RT Sfi21-like Siphoviridae in lactic acid bacteria."; J. Bacteriol. 184:6026-6036 (2002).
RN (8)
RP SEQUENCE FROM N.A.
RA Garcia P., Ladero V., Suarez J.E.;
RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251789; CAB63672.1; -
DR InterPro; IPR004968; Pox D5.
DR InterPro; IPR006500; Primase_C.
DR Pfam; PF03288; Pox D5; 1.
DR TIGRfam; TIGR01613; primase_Cterm; 1.
SQ SEQUENCE 770 AA; 88233 MW; 382B4F853010DCB CRC64;

Query Match 76.8%; Score 43; DB 2; Length 770;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYSKLPWT 9
|:|:|:|:
Db 27 HKYTKIPWS 35

RESULT 3

AAR11015
ID AAR11015 PRELIMINARY; PRT; 107 AA.
AC AAR11015;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE ANA Immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1e1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1e1 mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436855; AAR11015.1; -
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11408 MW; 0AAFB831B786EAFD CRC64;

Query Match 73.2%; Score 41; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPWT 9
|:|:|:|:
Db 82 HQWSSYPWT 90

RESULT 4
O6BN22
ID O6BN22 PRELIMINARY; PRT; 572 AA.
AC O6BN22;
DT 01-OCT-2004 (TREMBLrel. 28, Created)
DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similarities with sp|P47168 Saccharomyces cerevisiae YXR136C.
GN ORFNames=DEHAOF01045g;
OS Debaryomyces hansenii (Yeast) (Torulaopora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=4959;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marcq C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissrame A., Boyer J., Cattolico L., Confantolero F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogiropoulos O.,
RA Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Pukhina M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliardin C., Weisenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44 (2004).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382138; CAG88702.1; -
SQ SEQUENCE 572 AA; 65217 MW; 73D939503DEB2E8D CRC64;

Query Match 73.2%; Score 41; DB 2; Length 572;

Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOXSCLPMT 9
Db 155 HNHKLPMT 163

RESULT 5
O8XVB0 PRELIMINARY; PRT; 623 AA.

AC O8XVB0
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE PROBABLE GAMMA-GLUTAMYLTRANSPETIDASE PROTEIN (EC 2.3.2.2).
GN Name=ggf2; Synonyms=RS00172; OrderedLocustNames=RS0221;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Burkholderiaceae; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brotter P., Camus J.C., Catolico L.,
RA Chandler M., Choine N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigler P., Thibault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502(2002).
DR EMBL; AL646072; CAD16628.1; -.
DR MEROPS; T03.001; -.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0003840; F:gamma-glutamyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000101; GGT peptidase.
DR Pfam; PF01019; G-Glu transpept; 1.
DR PRINTS; PR01210; GGTTRANSPTASZ.
DR Acyltransferase; Complete proteome; Transferase.
KW ACyltransferase; Complete proteome; Transferase.
SQ SEQUENCE 623 AA; 65009 MW; 2201015F85FEA576 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 623;
Best Local Similarity 75.0%; Pred. No. 1,1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 OXSCLPMT 9
Db 181 RYKCLPMT 188

RESULT 6
K1R_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410393;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC against 3,4-pyruvylated galactose and isolated from a patient with
CC Waldenstrom's macroglobulinemia.
DR PIR; A01876; KJHWE.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 69.6%; Score 39; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 OXSCLPMT 9
Db 90 QXSFPMT 97

RESULT 7
O8YSAO PRELIMINARY; PRT; 258 AA.
AC O8YSAO;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Beta-carotene ketolase.
GN OrderedLocustNames=alx13189;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AF003592; BAB74888.1; -.
DR PIR; AF2204; AF2204.
DR GO; GO:0016701; P:oxidoreductase activity; acting on single d. . .; IEA.
DR GO; GO:0016119; P:carotene metabolism; IEA.
DR InterPro; IPR011393; Carotene ketolase.
DR InterPro; IPR005804; PA_decat.
DR InterPro; IPR010257; PA_decat.
DR Pfam; PF00487; PA_decatase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR ProDom; PD001081; PA_decat_sub; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 30313 MW; 8F8C8AECF8FE1B CRC64;

Query Match 69.6%; Score 39; DB 2; Length 258;
Best Local Similarity 62.5%; Pred. No. 71;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSLPWP 8
|:|:|
Db 240 HEYPOLPWP 247

RESULT 8
Q9VST8 PRELIMINARY; PRT; 351 AA.

AC Q9VST8; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C94942-PA (IDJ35503p) .
GN ORFNames=C94942;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_Taxid=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazer R.G., Chame M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abell J.F., Agbayani A., An H.J., Andrews-Plannkoch C., Baldwin D.,
RA Bailly R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cwley S., Dahke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mleishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheefel F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupel M.P., Smith T.,
RA Spier E., Spralling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.",
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.",

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.,
RT "The transposable elements of the Drosophila melanogaster euchromatic
genome: a genomic perspective.",
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.",
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Gartin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Paclet J., Paragov V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the OXA1/oxaA family.
DR EMBL; AF003553; AAF50323.1; -;
DR EMBL; AY069618; AAL39763.1; -;
DR InAct; Q9VST8; -;
DR FLYBASE; FBgn0035960; C94942.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0007165; P-signal transduction; IEA.
DR InterPro; IPR001708; 60kDa_innermed.
KW Transmembrane.
SQ SEQUENCE 351 AA; 39295 MW; C9C4469BF750FF1E CRC64;
Query Match 69.6%; Score 39; DB 2; Length 351;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSLPWP 8
|:|:|
Db 79 HDYSLPWP 86

RESULT 9
Q9X8FO PRELIMINARY; PRT; 288 AA.

AC Q9X8FO; 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative phosphotransferase.
GN OrderdocusNames=SC03277; ORFNames=SCE39.276;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/41711a1;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kiezer H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Croun A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kiezer T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinovitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939115; CAB4035.1; -.
 DR PIR; T36237; T36237.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR InterPro; IPR002575; APH trans.
 DR InterPro; IPR011009; Kinase-like.
 DR Pfam; PF01636; APH; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 288 AA; 31415 MW; 40B5BC848A42B5C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 288;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
 Db 256 HYVSDLPW 263

RESULT 10
 ID Q7NAA3 PRELIMINARY; PRT; 336 AA.
 AC Q7NAA3;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Complete genome; segment 1/17.
 GN OrderedLocustNames=plu0031;
 OS Photorhabdus luminescens (subsp. laumondii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 OX NCBI_TaxID=141679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TT01;
 RX MEDLINE=22937627; PubMed=14528314;
 RA Duchaud E., Runnick C., Frangeul L., Buchrieser C., Givaudan A.,
 RA Taouit S., Bocs S., Bouraux-Bude C., Chandelier M., Chatter J.-F.,
 RA Dassa E., Derose R., Deruelle S., Freysinet G., Gaudreau S.,
 RA Zouine M., Lancia A., Powell K., Stiguer P., Vincent R., Wingate V.,
 RA "The genome sequence of the entomopathogenic bacterium Photorhabdus
 luminescens";
 RT Nat. Biotechnol. 21:1307-1313(2003).
 RL Nat. Biotechnol. 21:1307-1313(2003).
 DR EMBL; BX571859; CAE12326.1; -.
 DR Photoblast; plu0031; -.
 DR InterPro; IPR000276; GPCR Rhodosp.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 336 AA; 38412 MW; 7EB8746696E2B8B6 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 336;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 QYSKLPWT 9

Db 104 QYHNLPT 111

RESULT 11
 ID Q9GKJ6 PRELIMINARY; PRT; 349 AA.
 AC Q9GKJ6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Butyrylcholinesterase (Fragment).
 GN Name=BCH;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21419000; PubMed=11528129;
 RA Van Poucke M., Verle M., Tuggle C., Plum F., Genet C.,
 RA Van Zeveren A., Peelman L.J.;
 RT "Integration of porcine chromosome 13 maps."
 RL Cytogenet. Cell Genet. 93:297-303(2001).
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AF222914; AAG41127.1; -.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004104; F:cholinesterase activity; IEA.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser_ester.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PRO0878; CHOLINESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 FT NON_TER 1 1
 FT NON_TER 349 349
 SQ SEQUENCE 349 AA; 39061 MW; D66354B14725B58 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 349;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
 Db 311 HRSKLPW 318

RESULT 12
 ID O13629 PRELIMINARY; PRT; 363 AA.
 AC O13629;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DE LIPOTE-PROTEIN LIGASE A (SPBC17A3.09c protein) (P1037 protein).
 GN Name=PL037; Synonym=SPBC17A3.09c;
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
 OX Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972 h-;
 RX MEDLINE=20089027; PubMed=10620777;
 RA Machida M., Yamazaki S., Kunihito S., Tanaka T., Kuehida N., Jinno K.,
 RA Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
 RA Sakai M., Aoki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q.,
 RA Yanagida M.;
 RT "A 38 kb segment containing the cdc2 gene from the left arm of fission
 yeast chromosome II: sequence analysis and characterization of the
 genomic DNA and cDNAs encoded on the segment.";
 RL Yeast 16:71-80(2000).

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972 h-;
RA Director-General of Biotechnology Center, Kuehida N., Machida M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Collins M., Brown D., Brown S., Chillingworth T., Churcher C.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsals K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
RA Wellens I., Vanscreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Dehrach H., Reinhardt R.,
RA Fohl T.M., Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
RA Goffeau A., Cadieu E., Driano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucan M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
DR EMBL; AB004537; BAA21417.1; -
DR EMBL; AL096552; CAB51768.1; -
DR PIR; T39701; T39701.
DR GenBank; SPombe; SPBC17A3.09c; -
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR004143; BPL_LiPA_LiPB.
DR InterPro; IPR004562; Lipolytrans.
DR Pfam; PF03099; BPL_LiPA_LiPB.1.
DR TrIRPfam; TrIRF00545; Lipolytrans; 1.
DR TrIRPfam; TrIRF00545; Lipolytrans; 1.
KW ligase.
SQ SEQUENCE 363 AA; 40651 MW; A6BF82EB7CB8EB13 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 363;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
| : |||
Db 322 HELLSIPWT 330

RESULT 13
Q6FOGO PRELIMINARY; PRT; 386 AA.
AC O6FOGO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Strain CBS138 chromosome 1 complete sequence.
GN ORFNames=CAGL0106534g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=5478;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;

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RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissarie A., Boyer J., Cattolico L., Confantolero F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaitre M., Lesur I., Ma L., Muller H.,
RA Micard J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Strub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Pukhara M., Thiery A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the OXA1/OXA family.
DR EMBL; CR380955; CAG60471.1; -
DR InterPro; IPR01708; 60kDa_innermem.
DR Pfam; PF02096; 60KD_IMP; 1.
KW Transmembrane.
SQ SEQUENCE 386 AA; 43188 MW; 55DBD0BC41423962 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 386;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
| : |||
Db 110 HAYSGLPW 117

RESULT 14
Q89UG7 PRELIMINARY; PRT; 389 AA.
AC Q89UG7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter permease protein.
GN OrderedOcunNames=blt1450;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_Taxid=375;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyumi T.,
RA Sasamoto S., Matsumura A., Ideasa K., Iriyuchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005940; BAC46715.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR01851; Bac_innermem_transp.
DR Pfam; PF02653; BPD_transp_2; 1.
KW Complete proteome.
SQ SEQUENCE 389 AA; 42197 MW; 2C7D90C36B8B1B26 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8
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DB 117 YSKLPW 122

RESULT 15

075885 PRELIMINARY; PRT; 434 AA.

AC 075885; 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE ADL315CP. 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

GN ADL315CP.

OS Ashbya gossypii (yeast) (Eremothecium gossypii).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

CC Saccharomycetales; Saccharomycetaceae; Eremothecium.

OK NCBI_TaxID=33169;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 10895;

RA Voegel S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE016889; AAS51605.1; -

DR AGD: ADL315C; -

DR InterPro: IPR010109; Kinase, like.

DR InterPro: IPR000719; Prot_Kinase.

DR InterPro: IPR002290; Ser_thr_kinase.

DR InterPro: IPR008271; Ser_thr_kin_AS.

DR InterPro: IPR001245; Tyr_kinase.

DR Pfam: PF00069; Pkinase; 1.

DR ProDom: PD000001; Prot_Kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR SMART; SM00219; TYKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.

KM ATP-binding; Kinase; Transferase.

SQ SEQUENCE 434 AA; 49672 MW; E3F62F511479CF1B CRC64;

Query Match 67.9%; Score 38; DB 2; Length 434;

Best Local Similarity 71.4%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPW 8

DB 326 QYAKIPW 332

RESULT 16

AAS51605 PRELIMINARY; PRT; 434 AA.

AC AAS51605; 23-APR-2004 (TREMBlrel. 27, Created)

DT 23-APR-2004 (TREMBlrel. 27, Last sequence update)

DE ADL315CP. 23-APR-2004 (TREMBlrel. 27, Last annotation update)

GN ADL315CP.

OS Ashbya gossypii (Yeast) (Eremothecium gossypii).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

CC Saccharomycetales; Saccharomycetaceae; Eremothecium.

OK NCBI_TaxID=33169;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 10895;

RA Voegel S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE016889; AAS51605.1; -

SQ SEQUENCE 434 AA; 49672 MW; E3F62F511479CF1B CRC64;

Query Match 67.9%; Score 38; DB 2; Length 434;

Best Local Similarity 71.4%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPW 8

DB 326 QYAKIPW 332

RESULT 17

CHLB_RABIT STANDARD; PRT; 581 AA.

AC P21977; 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)

DE (Choline esterase II) (Butyrylcholine esterase)

DE (Pseudocholinesterase).

GN Name=BCH; 05

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OK NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=New Zealand;

RA MEDLINE=90326526; PubMed=2374720;

RA Jbllo O., Roudani S., Chatonnet A.;

RT "Complete sequence of rabbit butyrylcholinesterase.";

RL Nucleic Acids Res. 18:3990-3990(1990).

RN [2]

RP SEQUENCE OF 75-215 FROM N.A.

RC TISSUE=Liver;

RA MEDLINE=91201348; PubMed=2016308;

RA Arpaug M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,

RA Barthelemy C.F., Nogueira C.P., la Du B.N., Lockridge O.;

RT "Use of the polymerase chain reaction for homology probing of

RT butyrylcholinesterase from several vertebrates.";

RL J. Biol. Chem. 266:6966-6974(1991).

CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2O) = choline + a

CC carboxylic acid anion.

CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The

CC two subunits in a dimer are linked by a disulfide bond.

CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.

CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with

CC organophosphate esters.

CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

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CC or send an email to license@isb-sib.ch).

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CC -----
DR EMBL; X52090; CAA36308.1; -.
DR EMBL; X52091; CAA36308.1; JOINED.
DR EMBL; X52092; CAA36308.1; JOINED.
DR EMBL; X62779; AAA31169.1; -.
DR PIR; S10255; C39768.
DR HSP; P22303; IFRU.
DR InterPro; IPR002018; CarbesteraeB.
DR InterPro; IPR000997; Cholinesterase.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Signal.
FT CHAIN 1 581
FT SIGNAL 1 8
FT ACT_SITE 205 205 Acyl-ester intermediate (by similarity).
FT ACT_SITE 332 332 Charge relay system (by similarity).
FT ACT_SITE 445 445 Charge relay system (by similarity).
FT DISULFID 72 99 By similarity.
FT DISULFID 259 270 By similarity.
FT DISULFID 407 526 By similarity.
FT DISULFID 578 578 Interchain (by similarity).
FT CARBOHYD 64 64 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 248 248 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 263 263 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 348 348 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 462 462 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 488 488 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 492 492 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 493 493 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 581 AA; 66156 MW; FE8B199E7B32EB0A CRC64;

Query Match 67.9%; Score 38; DB 1; Length 581;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HQYSKLPW 8
Db 430 HRSKLPW 437

RESULT 18
O9JKC1 PRELIMINARY; PRT; 597 AA.
ID O9JKC1;
AC O9JKC1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Butyrylcholinesterase.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Birmjoia S., Hinch S.H., Lockridge O., Hammond P.,
RA Birmjoia S., Hinch S.H., Lockridge O.,
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Tieu A.M., Lockridge O., Bartels C.F.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AF244349; AAF44713.1; -.
DR HSP; P22303; IFRU.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0004104; F: cholinesterase activity; IEA.
DR InterPro; IPR002018; CarbesteraeB.
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DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase.
SQ SEQUENCE 597 AA; 67776 MW; 771204D166C7EBAC CRC64;

Query Match 67.9%; Score 38; DB 2; Length 597;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HQYSKLPW 8
Db 446 HRSKLPW 453

RESULT 19
CHLE_HUMAN STANDARD; PRT; 602 AA.
ID CHLE_HUMAN
AC P06276;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Choline esterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Pseudocholesterase).
GN Name=BCH; Synonyms=CHE1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90212557; PubMed=232535;
RA Arpaug M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,
RA Lockridge O.;
RT "Structure of the gene for human butyrylcholinesterase. Evidence for a
RT single copy.";
RL Biochemistry 29:124-131(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal;
RX MEDLINE=87231856; PubMed=3035536;
RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreg H.;
RT "Isolation and characterization of full-length cDNA clones coding for
RT cholinesterase from fetal human tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88016155; PubMed=3477799;
RA McTiernan C., Atkins S., Chalonnet A., Vaughan T.A., Bartels C.F.,
RA Kott M., Roseberry T.L., la Du B.N., Lockridge O.;
RT "Brain cDNA clone for human cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villan D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman W., Madan A., Rodrigues S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shervencko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinska M.T., Skalska U., Smalins D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 29-602.
RC TISSUE=Plasma;
RX MEDLINE=87109144; PubMed=3542989;
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RL Johnson L.L.;
RT "Complete amino acid sequence of human serum cholinesterase.";
RL J. Biol. Chem. 262:549-557(1987).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=88007487; PubMed=3115973;
RA Lockridge O., Adkins S., la Du B.N.;
RT "Location of disulfide bonds within the sequence of human serum
RT cholinesterase.";
RL J. Biol. Chem. 262:12945-12952(1987).
RN [7]
RP REVIEW.
RX MEDLINE=89149758; PubMed=3067729;
RA Lockridge O.;
RT "Structure of human serum cholinesterase.";
RL Bioessays 9:125-128(1988).
RN [8]
RP VARIANT ATYPICAL GLY-98.
RX MEDLINE=89128896; PubMed=2915589;
RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA van der Spek A.F.L., Lockridge O., la Du B.N.;
RT "Identification of the structural mutation responsible for the
RT dibucaine-resistant (acyclic) variant form of human serum
RT cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN [9]
RP VARIANT ILE-358.
RX MEDLINE=96287386; PubMed=8680411;
RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA Motiwaki K.;
RT "Mutations of human butyrylcholinesterase gene in a family with
RT hypocholinesterasemia.";
RL Hum. Mutat. 6:349-351(1995).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- DISEASE: Mutant alleles of CHB1 are responsible for
CC hypocholinesterasemia resulting in succinethonium sensitivity.
CC Homozygous persons sustain prolonged apnea after administration of
CC the muscle relaxant succinethonium in connection with surgical
CC anaesthesia.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; M32391; AAA99296.1; -;
DR EMBL; M32389; AAA99296.1; JOINED.
DR EMBL; M32390; AAA99296.1; JOINED.
DR EMBL; M16541; AAA98113.1; -;
DR EMBL; M16474; AAA52015.1; -;

DR	EMBL; BC018141; AAH18141.1; ..
DR	PIR; A37699; ACBU.
DR	PDB; 1BRO; Model; A=30-560.
DR	PDB; 1EHQ; Model; A=30-560.
DR	PDB; 1P0I; X-ray; A=29-557.
DR	PDB; 1POM; X-ray; A=29-557.
DR	PDB; 1POP; X-ray; A=29-557.
DR	PDB; 1POJ; X-ray; A=29-557.
DR	GeneW; HGNC; 983; BCHE.
DR	MIM; 177400; ..
DR	GO; GO:0001540; P:beta-amylid binding; NAS.
DR	GO; GO:0003824; P:catalytic activity; NAS.
DR	GO; GO:0004104; F:cholinesterase activity; NAS.
DR	GO; GO:0019899; F:enzyme binding; NAS.
DR	GO; GO:0050783; P:cocaine metabolism; TMS.
DR	InterPro; IPR002018; Carbesterae8.
DR	InterPro; IPR000379; Ser estsr.
DR	Pfam; PF00135; Coesterase; 1.
DR	PRINTS; PR00878; CHOLINESTERASE.
DR	PROSITE; PS00122; CARBOXYLTERASE_B_1; 1.
DR	PROSITE; PS00941; CARBOXYLTERASE_B_2; 1.
KM	3D-structure; Direct protein sequencing; Disease mutation;
KM	Glycoprotein; Hydroxylase; Polymorphism; Serine esterase; Signal.
FT	SIGNAL 1 28
FT	CHAIN 29 602
FT	ACT_SITE 226 226
FT	ACT_SITE 353 353
FT	ACT_SITE 466 466
FT	DISELFID 93 120
FT	DISELFID 280 291
FT	DISELFID 428 547
FT	DISELFID 599 599
FT	CARBOXHD 45 45
FT	CARBOXHD 85 85
FT	CARBOXHD 134 134
FT	CARBOXHD 269 269
FT	CARBOXHD 284 284
FT	CARBOXHD 369 369
FT	CARBOXHD 483 483
FT	CARBOXHD 509 509
FT	CARBOXHD 514 514
FT	VARIANT 98 98
FT	VARIANT 271 271
FT	VARIANT 358 358
FT	VARIANT 418 418
FT	VARIANT 567 567
SEQ	SEQUENCE 602 AA; 68418 MM; C9834509D9057F27 CRC64; Query Match 67.9%; Score 38; DB 1; Length 602; Best Local Similarity 75.0%; Prec. No. 2.5e+02; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	1 HOYSKLPWF 8 : Db 451 HRSSKLPWF 458
RESULT 20	
ID	CHLE MOUSE STANDARD; PTR; 603 AA.
AC	003311;
DT	01-OCT-1993 (Rel. 27, Created)
DT	01-OCT-1993 (Rel. 27, Last sequence update)
DT	01-OCT-2004 (Rel. 45, Last annotation update)
DE	Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)

DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholesterase).
OS Name=Bche;
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90380429; PubMed=2400605;
RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
RN [2]
RP SEQUENCE OF 97-237 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpaugh M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL: M99492; AAA37328.1; -.
DR PIR: S70849; S70849.
DR HSSP: P22303; 1PBU.
DR MGD: MGI:894278; Bche.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser. esters.
DR Pfam: PF00135; COESTERASE_1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 29
FT CHAIN 30 603 Cholinesterase.
FT ACT_SITE 227 227 Acyl-ester intermediate (By similarity).
FT ACT_SITE 354 354 Charge relay system (By similarity).
FT ACT_SITE 467 467 Charge relay system (By similarity).
FT DISULFID 94 121 By similarity.
FT DISULFID 281 292 By similarity.
FT DISULFID 429 548 By similarity.
FT DISULFID 600 600 Interchain (By similarity).
FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 510 510 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 515 515 N-linked (GlcNAc...) (Potential).
FT CONFLICT 129 129 R -> P (in Ref. 2).
SQ SEQUENCE 603 AA; 68521 MW; 719B1B220D1E5367 CRC64;

Query Match Score 38; DB 1; Length 603;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HOYSKLPW 8
|:|||||
Db 452 HRSSKLPW 459

RESULT 21
ID Q90ZK8 PRELIMINARY; PRT; 603 AA.
AC Q90ZK8;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Butyrylcholinesterase precursor (EC 3.1.1.8).
GN Name=Bche;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Geisler K., Chatonnet A., Layer P.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL: AJ306928; CAC37792.1; -.
DR HSSP: P21836; 1NSW.
DR GO: GO:0004104; F:cholinesterase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser. esters.
DR Pfam: PF00135; COESTERASE_1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 603 butyrylcholinesterase.
SQ SEQUENCE 603 AA; 68480 MW; A350FDDF68574ADF CRC64;

Query Match Score 38; DB 2; Length 603;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HOYSKLPW 8
|:|||||
Db 451 HRSSKLPW 458

RESULT 22
ID BAC34196 PRELIMINARY; PRT; 603 AA.
AC BAC34196;
DT 14-APR-2004 (TREMblrel. 27, Created)
DT 14-APR-2004 (TREMblrel. 27, Last sequence update)
DT 14-APR-2004 (TREMblrel. 27, Last annotation update)
DE Adult male liver tumor cDNA, RIKEN full-length enriched library,
clone: C730038G20 product: butyrylcholinesterase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
Nature 420:563-573 (2002)."
RL


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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=2049374; PubMed=11042159;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
  Kono H., Akiyama J., Nishi K., Kikunishi T., Tahtiro H., Itoh M.,
  Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1157-1171(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
  Hayashida K., Hayatsu N., Hiramoto K., Hiraga I., Kasukawa T.,
  Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kikunishi T.,
  Katoh H., Kawai T., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
  Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
  Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y.,
  Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
  Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
  Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
  Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (Jul-2001) to the EMBL/GenBank/DBJ database.
RL EMBL; AK050337; BNC34196.1; -;
SQ SEQUENCE 603 AA; 68462 MW; 2CB79C46797B3713 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 603;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
Db 452 HRSSKLPW 459

RESULT 23
Q6MI24 PRELIMINARY; PRT; 657 AA.
ID Q6MI24;
AC Q6MI24;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor (EC 3.6.3.14).
GN OrderedLocusName=Bd3355;

```

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OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
ON NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;
RA Rendall S., Jagtap P., Rosinus A., Eppinger M., Baar C.,
  Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
  Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
  genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842655; CAE78158.1; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
KW Complete proteome; Hydrolase; Hypothetical protein; Signal.
FT SIGNAL
SQ SEQUENCE 657 AA; 74124 MW; B3C8FA18D745419C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 657;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPW 8
Db 455 EYSKLPW 461

RESULT 24
Q8MT38 PRELIMINARY; PRT; 657 AA.
ID Q8MT38;
AC Q8MT38;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor (EC 3.6.3.14).
GN BD3355.
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
ON NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;
RA Rendall S., Jagtap P., Rosinus A., Eppinger M., Baar C.,
  Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
  Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
  genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842655; CAE78158.1; -;
KW Hydrolase; Hypothetical protein; Signal.
FT SIGNAL
SQ SEQUENCE 657 AA; 74124 MW; B3C8FA18D745419C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 657;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPW 8
Db 455 EYSKLPW 461

RESULT 25
Q8MT38 PRELIMINARY; PRT; 698 AA.
ID Q8MT38;
AC Q8MT38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```

DE Gag-like protein.
 GN Name=ORF1;
 OS Papilio xuthus.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Papilionidae; Papilioninae; Papilio.
 NCBI_TaxID=66420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22511580; PubMed=12644555;
 RA Kojima K.K., Fujiwara H.;
 RT "Evolution of target specificity in R1 clade non-LTR
 retrotransposons."
 RL Mol. Biol. Evol. 20:351-361 (2003).
 DR EMBL; AB078928; BAC06449.1;
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zfc_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; ZNF_C2HC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 SQ SEQUENCE 698 AA; 75954 MW; E10A65A5A6F90A5 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 698;
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOXSXLPT 9
 Db 375 HOXKELPT 383

RESULT 26

06CY8 PRELIMINARY; PRT; 1036 AA.

AC 06CY8;
 DT 01-OCT-2004 (TEMBLrel. 28, Created)
 DT 01-OCT-2004 (TEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE Strain NRRL Y-1140 chromosome F of strain NRRL Y-1140 of Kluyveromyces
 lactis.
 GN ORFNames=K1LA0P149279;
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG GENOLEVURES;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Ajie M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boistrame A., Boyer J., Catolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikoleki M., Ozias S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Sveinene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44 (2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382126; CAG98459.1;
 SQ SEQUENCE 1036 AA; 118499 MW; 22DF98B5DBF3705C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 1036;
 Best Local Similarity 55.6%; Pred. No. 4.4e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOXSXLPT 9
 Db 571 HFYKVPWS 579

RESULT 27

MCE.REOVD STANDARD; PRT; 1289 AA.

AC P11079;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE mRNA capping enzyme (mRNA guanylyltransferase) (EC 2.7.7.50) (GTP--RNA
 DE guanylyltransferase).
 GN Name=L2;
 OS Reovirus type 3 (strain Dearing) (T3D).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 NCBI_TaxID=10886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88058999; PubMed=2824487;
 RA Seltzer L.S., Zheng K., Shatkin A.J.;
 RT "Complete nucleotide sequence of reovirus L2 gene and deduced amino
 RT acid sequence of viral mRNA guanylyltransferase."
 RL J. Biol. Chem. 262:16289-16293 (1987).
 CC -1- FUNCTION: mRNA capping.
 CC -1- CATALYTIC ACTIVITY: GTP + (5')ppp-mRNA = diphosphate +
 CC G(5')ppp-mRNA.
 CC CC

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DR EMBL; J03488; AAA47253.1; -.
 DR PIR; A28471; RXMR3.
 DR InterPro; IPR010311; Reovirus_L2.
 DR Pfam; PF06016; Reovirus_L2; 1.
 KM mRNA capping; mRNA processing; Nucleotidyltransferase; Transferase.
 FT DOMAIN 941 968 Hydrophilic
 SQ SEQUENCE 1289 AA; 14406 MW; 8C497F0B6937018B CRC64;

Query Match 67.9%; Score 38; DB 1; Length 1289;
 Best Local Similarity 66.7%; Pred. No. 5.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOXSXLPT 9
 Db 659 HOXSXLPT 667

RESULT 28

091RA1 PRELIMINARY; PRT; 1289 AA.

AC 091RA1;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Core-spike protein Lambda-2.
 OS Reovirus type 3 (strain Dearing) (T3D).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus;
 OC Mammalian orthoreoviruses.
 NCBI_TaxID=10886;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Hall;
 RX MEDLINE=21425393; PubMed=11531411;
 RA Brenz L.A., Broering T.J., McCutcheon A.M., Harrison S.J.,
 RA Luongo C.L., Nibert W.L.;
 RT "Mammalian reovirus L2 gene and lambda2 core spike protein sequences
 RT and whole-genome comparisons of reoviruses type 1 Lang, type 2 Jones,
 RT and type 3 Dealing.";
 RL Virology 287:333-348 (2001).
 DR EMBL; AF378010; AAK57514.1; -;
 DR InterPro: IPR010311; Reovirus_L2.
 DR Pfam; PF06016; Reovirus_L2; 1.
 SQ SEQUENCE 1289 AA; 143843 MW; EA1D962522E2B8F4 CRC64;

Query Match
 Best Local Similarity 66.7%; Score 38; DB 2; Length 1289;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
 DB 659 HOHSLTWT 667

RESULT 29

ID AAR11062 PRELIMINARY; PRT; 95 AA.
 AC AAR11062;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE ANA immunoglobulin kappa light chain (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S1el; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.S1el mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436902; AAR11062.1; -;
 FT NON_TER 1
 FT NON_TER 95
 SQ SEQUENCE 95 AA; 10220 MW; 680C89BE1C872248 CRC64;

Query Match
 Best Local Similarity 66.1%; Score 37; DB 2; Length 95;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
 DB 84 HOHSSCPWT 92

RESULT 30

ID AAR11071 PRELIMINARY; PRT; 99 AA.
 AC AAR11071;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE ANA immunoglobulin kappa light chain (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S1el; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.S1el mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436911; AAR11071.1; -;

FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10529 MW; BBC09D5304E08F98 CRC64;

Query Match
 Best Local Similarity 66.1%; Score 37; DB 2; Length 99;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 OYSKLPWT 9
 DB 88 QYQFPWT 95

RESULT 31

ID KVI1B_HUMAN STANDARD; PRT; 108 AA.
 AC P01554;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-1 region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
 RN [2]

RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlmayer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the Bence-
 RT Jones protein Au.";

RL Biophys. Struct. Mech. 1:139-146 (1975).
 CC -1- MISCELLANEOUS: The structure of the V region was determined by
 CC molecular replacement methods using the known structure of the V
 CC region of the kappa chain REI.
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91653; KIHUHU.
 DR PDB; 1JVS; X-ray; A=1-107.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.

FT DOMAIN 1
 FT DOMAIN 23
 FT DOMAIN 24
 FT DOMAIN 35
 FT DOMAIN 50
 FT DOMAIN 57
 FT DOMAIN 89
 FT DOMAIN 98
 FT DOMAIN 107
 FT DISULFID 23
 FT STRAND 4
 FT STRAND 10
 FT STRAND 13
 FT TURN 15
 FT TURN 19
 FT TURN 25
 FT TURN 30
 FT TURN 31
 FT TURN 33
 FT TURN 38
 FT TURN 41

Framework-1.
 Complementarity-determining-1.
 Framework-2.
 Complementarity-determining-2.
 Framework-3.
 Complementarity-determining-3.
 Framework-4.
 By similarity.

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FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 69
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6FB9 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
Db 90 QYDYLPT 97

RESULT 32
Q9CTV5 PRELIMINARY; PRT; 108 AA.
ID Q9CTV5;
AC Q9CTV5;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
DE library, clone:543043C04 product:hypothetical protein, full insert
DE sequence. (Fragment).
GN Name=543043C04Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA the FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
RA Kono H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and substructure of cap-trapper-selected cDNAs to
RT Prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;

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RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K.; Itoh M.; Aizawa K.; Nagaoka S.; Sasaki N.; Carninci P.;
RA Kono H.; Akiyama J.; Nishi K.; Kitsuai T.; Taahito H.; Itoh M.;
RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.;
RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;
RA Fujiwaka S.; Inoue K.; Ozawa Y.; Izawa M.; Ohara E.; Matsuki M.;
RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsura S.; Kawai J.;
RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J.; Aizawa K.; Akahira S.; Akimura T.; Arai A.; Aono H.;
RA Arakawa T.; Bono H.; Carninci P.; Fukuda S.; Furumishi Y.; Furuno M.;
RA Hanagaki T.; Hara A.; Hayatsu N.; Hiramoto K.; Hirooka T.; Hori F.;
RA Imotani K.; Ishii Y.; Itoh M.; Izawa M.; Kasukawa T.; Kato H.;
RA Kawai J.; Kojima Y.; Kono H.; Kouda M.; Koya S.; Kurihara C.;
RA Matsuyama T.; Miyazaki A.; Nishi K.; Nomura K.; Nunazaki R.; Ohno M.;
RA Okazaki Y.; Okido T.; Owa C.; Saito H.; Saito R.; Sakai C.; Sakai K.;
RA Sano H.; Sasaki D.; Shibata K.; Shibata Y.; Shingawa A.; Shiraki T.;
RA Sogabe Y.; Suzuki H.; Tagami M.; Tagawa A.; Takahashi F.; Tanaka T.;
RA Tejima Y.; Toya T.; Yamamura T.; Yasunishi A.; Yoshida K.; Yoshino M.;
RA Muramatsu M.; Hayashizaki Y.;
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK019949; BAB31930.1;
DR MGD; MGI:1925346; 543043C04Rik.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11561 MW; 8B2DBF61623608F CRC64;

Query Match 66.1%; Score 37; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
Db 17 QISRPLPT 24

RESULT 33
KVAC_HUMAN
ID KVAC_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P.; Mills F.; Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X02990; CAA26733.1; -.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR IMMUNOGLOBULIN V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Complementarity-determining-3.
FT DOMAIN 115 121 Framework-4.
FT DOMAIN 122 133 Complementarity-determining-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22F0738832 CRC64;

Query Match
Best Local Similarity 66.1%; Score 37; DB 1; Length 134;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 116 QYXNLPWT 123

RESULT 34
Q8VDDO PRELIMINARY; PRT; 134 AA.
ID Q8VDDO;
AC Q8VDDO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN Name=anti-MOG kappa;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Semb P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cheraiovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; A416331; CAC94866.1; -.
DR PIR; G27887; G27887.
DR HSSP; P01834; IMIM.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CFFD8E223682D0CF CRC64;

Query Match
Best Local Similarity 66.1%; Score 37; DB 2; Length 134;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPTW 9
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DB 110 HOSSYPWT 118

RESULT 35
ID 085999 PRELIMINARY; PRT; 190 AA.
AC 085999;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein orf1251 precursor.
GN Name=orf1251;
OS Spingomonas aromaticivorans.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Novosphingobium.
OX NCBI_TaxID=48935;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F199;
RX MEDLINE=99175459; Pubmed=10049392;
RA Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sisk E.C.,
RA Sensen C., Gaasterland T., Fredrickson J.K., Saffer J.D.,
RT "Complete sequence of a 184-kilobase catabolic plasmid from
RT Spingomonas aromaticivorans F199."
RL J. Bacteriol. 181:1585-1602(1999).
DR EMBL; AF079317; AAD04015.1; -.
DR PIR; T31291; T31291.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR006311; Tat.
DR TIGRPFAM; TIGR01409; Tat_signal_seg; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KM Hypothetical protein; Plasmid; Signal.
FT SIGNAL 1 31 Potential.
SQ SEQUENCE 190 AA; 20392 MW; 2FA2F9E979F9822 CRC64;

Query Match
Best Local Similarity 66.1%; Score 37; DB 2; Length 190;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPTW 8
DB 114 HOYKLRW 121

RESULT 36
Q9PU09 PRELIMINARY; PRT; 242 AA.
ID Q9PU09;
AC Q9PU09;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Dm20 (Fragment).
GN Name=Dm20;
OS Latimeria chalumnae (Latimeria) (Coelacanth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Coelacanthiformes; Coelacanthidae; Latimeria.
OX NCBI_TaxID=7897;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99310421; Pubmed=10403627;
RA Tohyama Y., Kasama-Yoshida H., Sakuma M., Kobayashi Y., Cao Y.,
RA Hasegawa M., Kojima H., Tamai Y., Tanokura M., Kurihara T.;
RT "Gene structure and amino acid sequence of Latimeria chalumnae
RT (Coelacanth) myelin Dm20: phylogenetic relation of the fish."
RL Neurochem. Res. 24:867-873(1999).
DR EMBL; AB025938; BAA84207.1; -.
DR EMBL; AB025933; BAA84207.1; JOINED.
DR EMBL; AB025934; BAA84207.1; JOINED.
DR EMBL; AB025935; BAA84207.1; JOINED.
DR EMBL; AB025936; BAA84207.1; JOINED.
DR EMBL; AB025937; BAA84207.1; JOINED.
```

DR InterPro; IPR001614; Myelin_PLP.
 DR Pfam; PF01275; Myelin_PLP; 1.
 DR PRINTS; PR00214; MYELINPLP.
 DR SMART; SM00002; PLP; 1.
 FT NON TER 1
 SQ SEQUENCE 242 AA; 26991 MW; 9BB3556B38F5DE2 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 242;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
 DB 168 QYGLPWT 175

RESULT 37
 Q8UT6 PRELIMINARY; PRT; 245 AA.
 AC Q8UT6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Dmalpahal.
 GN Name=PlpA;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Werner H., Schweitzer J., Schachner M., Nave K.-A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY070259; AAL59885.1; -;
 DR ZFIN; ZDB-GENE-001202-1; plpA.
 DR InterPro; IPR001614; Myelin_PLP.
 DR Pfam; PF01275; Myelin_PLP; 1.
 DR PRINTS; PR00214; MYELINPLP.
 DR SMART; SM00002; PLP; 1.
 DR PROSITE; PS01004; MYELIN_PLP_2; 1.
 SQ SEQUENCE 245 AA; 27510 MW; 764B19BF8B949C9A CRC64;

Query Match 66.1%; Score 37; DB 2; Length 245;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
 DB 171 QYGLPWT 178

RESULT 38
 Q6MOC7 PRELIMINARY; PRT; 330 AA.
 AC Q6MOC7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedlocusNames=Bd0547;
 OS Bdellovibrio bacteriovorus.
 OC Bacteria; Proteobacteria; Delta proteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OX NCBI_TaxID=959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasks: life cycle of Bdellovibrio bacteriovorus from a

RT genomic perspective."; Science 303:689-692(2004).
 RL EMBL; BX842647; CAE78520.1; -;
 DR EMBL; BX842647; CAE78520.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 330 AA; 37401 MW; E67D64135E164929 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 330;
 Best Local Similarity 62.5%; Pred. No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
 DB 207 NOTDKVFW 214

RESULT 39
 CAE78520 PRELIMINARY; PRT; 330 AA.
 AC CAE78520;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN BD0547.
 OS Bdellovibrio bacteriovorus.
 OC Bacteria; Proteobacteria; Delta proteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OX NCBI_TaxID=959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasks: life cycle of Bdellovibrio bacteriovorus from a
 RT genomic perspective."; Science 303:689-692(2004).
 RL EMBL; BX842647; CAE78520.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 330 AA; 37401 MW; E67D64135E164929 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 330;
 Best Local Similarity 62.5%; Pred. No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
 DB 207 NOTDKVFW 214

RESULT 40
 Q9FLA1 PRELIMINARY; PRT; 388 AA.
 AC Q9FLA1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Similarity to heat shock transcription factor.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98344145; PubMed=9679202;
 RA Kaneke T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
 RT features of the regions of 1,381,565 bp covered by twenty one
 RT physically assigned P1 and TAC clones."; DNA Res. 5:131-145(1998).

DR EMBL; AB010693; BAB10879.1; -.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR006566; FBD.
 DR InterPro; IPR008945; Skp1_Skp2.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SM00579; FBD; 1.
 DR PROSITE; PS50181; FBOX; 1.
 KW Heat shock.
 SO SEQUENCE 388 AA; 45144 MW; 3117852CD27D24F5 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 388;
 Best Local Similarity 75.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
 DB 256 HSYSKLGW 263

Search completed: December 17, 2004, 19:14:44
 Job time : 28.8989 secs

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QY 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFESHYAMSWVRQAPGKLEWVAYISSGSGCTYY 60
 |||
 DB 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFESHYAMSWVRQAPGKLEWVAYISSGSGCTYY 60
 |||
 QY 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
 |||
 DB 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
 |||

RESULT 2 ABU11010

ID ABU11010 standard; protein; 119 AA.

XX ABU11010;

XX 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated protein #3.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Synthetic.

XX WO200278739-A1.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-JP003170.

XX 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 8; Page 99; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC anticancer activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 CC

XX Sequence 119 AA;

XX Query Match 100.0%; Score 624; DB 6; Length 119;

XX Best Local Similarity 100.0%; Pred. No. 8.2e-50;

XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFESHYAMSWVRQAPGKLEWVAYISSGSGCTYY 60
 |||
 DB 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFESHYAMSWVRQAPGKLEWVAYISSGSGCTYY 60
 |||
 QY 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
 |||
 DB 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
 |||

RESULT 3 AAB81987

ID AAB81987 standard; protein; 582 AA.

XX AAB81987;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX Synthetic.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

XX 06-APR-2000; 2000JP-00105086.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.

XX Claim 41; Page 168-172; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumours, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC

XX Sequence 582 AA;

XX Query Match 100.0%; Score 624; DB 4; Length 582;

XX Best Local Similarity 100.0%; Pred. No. 4.3e-49;

XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFESHYAMSWVRQAPGKLEWVAYISSGSGCTYY 60
 |||
 DB 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFESHYAMSWVRQAPGKLEWVAYISSGSGCTYY 60
 |||
 QY 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
 |||
 DB 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
 |||

RESULT 4 AAB81989

ID AAB81989 standard; protein; 119 AA.

XX AAB81989;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX Mus musculus.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

```

XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
PI Hanai N, Shitara K, Nakamura K, Niwa R,
XX WPI; 2001-266143/27.
DR
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Claim 10; Page 173-174; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 119 AA;

Query Match          92.8%; Score 579; DB 4; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.1e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 EVQLVESGDDFVQPGGSLRVSCAAGFAFSAHVMWVRQAPGKLEWVAIYSSGSGTTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EYTLVESGDDFVQPGGSLRVSCAAGFAFSAHVMWVRQAPKRLWVAIYSSGSGTTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
ABU1012
ID ABU1012 standard; protein; 119 AA.
XX
XX ABU1012;
AC
XX
DT 04-FEB-2003 (first entry)
XX
DE Modified ganglioside GD3 antibody associated protein #5.
XX
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX Mus musculus.
OS
XX WO200278739-A1.
PN
XX 10-OCT-2002.
PD
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX 29-MAR-2001; 2001JP-00097483.
PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX WPI; 2003-067410/06.
DR
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Claim 7, Page 112-113; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
CC

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```

CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX
SQ Sequence 119 AA;

Query Match          92.8%; Score 579; DB 6; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.1e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 EVQLVESGDDFVQPGGSLRVSCAAGFAFSAHVMWVRQAPGKLEWVAIYSSGSGTTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EYTLVESGDDFVQPGGSLRVSCAAGFAFSAHVMWVRQAPKRLWVAIYSSGSGTTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
AAR33256
ID AAR33256 standard; protein; 130 AA.
XX
XX AAR33256;
AC
XX
DT 25-MAR-2003 (revised)
DT 12-JUL-1993 (first entry)
XX
XX
DE Rat immunoglobulin H chain variable region of pK4641HA3.
XX
XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
XX humanised; chimeric; antibody; expression vector.
XX
XX Rattus rattus.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..10 "Signal peptide"
FT Protein 11..130
FT Protein /note= "Mature protein"
XX
XX EP533199-A2.
PN
XX 24-MAR-1993.
PD
XX 18-SEP-1992; 92EP-00116026.
PF
XX 18-SEP-1991; 91JP-00238375.
PR
XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.
PA
PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX WPI; 1993-095510/12.
DR
XX N-PSDB; AA033257.
DR
XX
XX Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
XX cancers, such as melanoma, neuroblastoma, etc.
XX
XX Claim 6; Page 29-30; 63pp; English.
XX
XX The sequences given in AAR33256-57 represent rat heavy and light chain
XX variable regions respectively. The DNA sequences encoding these proteins
XX were used in the construction of humanised chimeric antibody expression
XX vectors. In these humanised antibodies none of the amino acids of the non
XX -human animal Ab variable region have been changed. (Updated on 25-MAR-
XX 2003 to correct FN field.)
XX
XX Sequence 130 AA;
SQ

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```
Query Match          92.8%; Score 579; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 1.2e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGCTTY 60
DB 11 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQTPARKLEWVAYISSGSGCTTY 70

QY 61 SDSVKGRFTTISRDNASKNTLYLQWRSLRAEDSAVYFCTRYKLGTYYPDSSWGQTTLTVSS 119
DB 71 SDSVKGRFTTISRDNASKNTLYLQWRSLRSEDSAMVFCTRYKLGTYYPDSSWGQTTLTVSS 129

RESULT 7
AAR53341
ID AAR53341 standard; protein; 130 AA.
XX
AC AAR53341;
XX
DE 18-NOV-1994 (first entry)
XX
DE KM641 L chain variable region.
XX
KM Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KM expression vector; heavy; light; chain; hypervariable region; CDR;
KM constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= sig_peptide
XX
PN AU9346181-A.
XX
PD 17-MAR-1994.
XX
PF 07-SEP-1993; 93AU-00046181.
XX
PR 07-SEP-1992; 92JP-00238452.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
DR WPI; 1994-126857/16.
DR N-PSDB; AAQ45439.
XX
PT Humanised antibody specific for ganglioside GM2 - used for producing a
PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX
PS Example 2; Page 116-117; 191pp; English.
XX
CC Example 2 describes the construction of the vector pCh1641HA1 for
CC chimeric human antibody H chain expression. mRNA from mouse anti-CD3
CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
CC was constructed by joining the H chain variable region gene from
CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
CC synthetic DNAs given in AAQ63439 and AAQ63440
XX
SQ Sequence 130 AA;

Query Match          92.8%; Score 579; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 1.2e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGCTTY 60
DB 11 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQTPARKLEWVAYISSGSGCTTY 70
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QY 61 SDSVKGRFTTISRDNASKNTLYLQWRSLRAEDSAVYFCTRYKLGTYYPDSSWGQTTLTVSS 119
DB 71 SDSVKGRFTTISRDNASKNTLYLQWRSLRSEDSAMVFCTRYKLGTYYPDSSWGQTTLTVSS 129

RESULT 8
AAI28369
ID AAI28369 standard; protein; 130 AA.
XX
AC AAI28369;
XX
DE 04-NOV-1999 (first entry)
XX
DE pKM641 HA3 immunoglobulin heavy chain.
XX
KM antibody; nucleotide; genomic; hypervariable region; chimeric;
KM light chain; amino acid.
XX
OS Mus sp.
XX
PN USS939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-00483528.
XX
PR 07-SEP-1993; 93US-00116778.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
DR WPI; 1999-468416/39.
DR N-PSDB; AAX99482.
XX
PT Chimeric human antibody expression vectors.
XX
PS Example 1; Col 99-101; 188pp; English.
XX
CC This immunoglobulin region was isolated from pKM641HA3. This sequence has
CC no methionine initiation codon and the leader sequence was partly
CC lacking. The chimeric human antibodies are useful in the treatment of
CC cancer, especially that which is of neural ectodermal origin. In contrast
CC to prior art constructs based on mouse monoclonal antibodies, the
CC chimeric human antibodies do not cause anti-mouse immunoglobulin
CC production. The chimeric human antibodies have a prolonged half-life and
CC a reduced frequency of adverse effects when compared to mouse monoclonal
CC antibodies
XX
SQ Sequence 130 AA;

Query Match          92.8%; Score 579; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 1.2e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGCTTY 60
DB 11 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQTPARKLEWVAYISSGSGCTTY 70

QY 61 SDSVKGRFTTISRDNASKNTLYLQWRSLRAEDSAVYFCTRYKLGTYYPDSSWGQTTLTVSS 119
DB 71 SDSVKGRFTTISRDNASKNTLYLQWRSLRSEDSAMVFCTRYKLGTYYPDSSWGQTTLTVSS 129

RESULT 9
AAB01627
ID AAB01627 standard; protein; 130 AA.
XX
AC AAB01627;
XX
DE 07-DEC-2000 (first entry)
XX
```

DE Murine immunoglobulin heavy chain variable region.
 XX
 XX Mouse; immunoglobulin, H chain; heavy chain; variable region; cancer;
 KM humanised antibody.
 XX
 XX Mus sp.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..10
 FT /label= signal_peptide
 FT 11..130
 FT /label= mature_immunoglobulin_heavy_chain_variable region
 FT
 XX
 XX EP1013761-A2.
 PN
 XX
 XX PD 28-JUN-2000.
 XX
 XX PF 18-SEP-1992; 99EP-00124345.
 XX
 XX PR 18-SEP-1991; 91JP-00238375.
 XX
 XX PR 18-SEP-1992; 92EP-00116026.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
 PI
 XX WPI: 2000-402204/35.
 DR N-PSDB; AAB51003.
 XX
 XX PT New humanised chimera antibody KM-871 useful for treating cancer,
 PT comprises variable region of mouse monoclonal antibody, reactive with
 PT ganglioside and human antibody constant region.
 PT
 XX Claim 14; Page 27-28; 65pp; English.
 PS
 XX
 XX The present sequence is a murine immunoglobulin heavy chain variable
 CC region from plasmid KM-641. The coding sequence was used in the creation
 CC of an expression vector, along with the sequence for a human antibody, to
 CC produce humanised chimaeric antibodies, which can be used to treat
 CC cancer. Humanised chimaeric antibodies are more effective than mouse
 CC antibodies as they do not provoke a reaction in the human and side
 CC effects, such as the formation of anti-mouse immunoglobulin antibody and
 CC the rapid half-life of the immunoglobulins, do not occur
 CC
 XX
 XX Sequence 130 AA;
 SQ
 Query Match 92.8%; Score 579; DB 3; Length 130;
 Best Local Similarity 91.6%; Pred. No. 1.2e-45;
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EVQLVSSGDPFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAIYISGGSGTTY 60
 DB 11 EVTLVSSGGDFVPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLVWVAIYISGGSGTTY 70
 QY 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 119
 OS 71 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 129
 DB
 RESULT 10
 AAB81977
 ID AAB81977 standard; protein; 138 AA.
 XX
 XX AAB81977;
 AC
 XX
 XX 03-JUL-2001 (first entry)
 DT
 XX
 XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.
 DE
 XX Ganglioside, GD3; complementarity determining region; CDR; antibody;
 KM cancer.
 XX
 XX Mus musculus.
 OS

XX
 PN WO200123432-A1.
 XX
 XX 05-APR-2001.
 PD
 XX
 XX 29-SEP-2000; 2000MO-JP006774.
 PF
 XX
 XX 30-SEP-1999; 99JP-00278291.
 PR
 XX 06-APR-2000; 2000JP-00105088.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 PI
 XX WPI: 2001-266143/27.
 DR
 XX
 XX PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 PT
 XX Example 1; Page 138-139; 183pp; Japanese.
 PS
 XX
 XX The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC
 XX
 XX Sequence 138 AA;
 SQ
 Query Match 92.8%; Score 579; DB 4; Length 138;
 Best Local Similarity 91.6%; Pred. No. 1.3e-45;
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EVQLVSSGDPFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAIYISGGSGTTY 60
 DB 20 EVTLVSSGGDFVPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLVWVAIYISGGSGTTY 79
 QY 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 119
 OS 80 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 138
 DB
 RESULT 11
 ABU11002
 ID ABU11002 standard; protein; 138 AA.
 XX
 XX ABU11002;
 AC
 XX
 XX 04-FEB-2003 (first entry)
 DT
 XX
 XX Modified ganglioside GD3 antibody associated protein #1.
 DE
 XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 KM
 XX Mus musculus.
 OS
 XX WO200278739-A1.
 FN
 XX
 XX 10-OCT-2002.
 PD
 XX
 XX 29-MAR-2002; 2002MO-JP003170.
 PF
 XX
 XX 29-MAR-2001; 2001JP-00097483.
 PR
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Shitara K, Niwa R, Kanazawa J, Asada M;
 PI
 XX WPI: 2003-067410/06.
 DR
 XX
 XX Drugs containing genetically-modified antibody against ganglioside GD3,
 PT

PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
PS Example 3; Page 97; 121pp; Japanese.
XX
CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ Sequence 138 AA;

Query Match 92.8%; Score 579; DB 6; Length 138;
Best Local Similarity 91.6%; Pred. No. 1.3e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVLVSSGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLWVAYISSGSGTTY 60
Db 20 EYTLVSSGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPARLEWVAYISSGSGTTY 79

Qy 61 SDSVKGRFTISRDNASKNTLYLQWRSIRAPDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
Db 80 SDSVKGRFTISRDNASKNTLYLQWRSIRSEDSAMVFCTRVKGTYYPDSWGQGTLLTVSS 138

RESULT 12
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 39; Page 175-179; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;

Query Match 92.8%; Score 579; DB 4; Length 582;
Best Local Similarity 91.6%; Pred. No. 6e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVLVSSGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLWVAYISSGSGTTY 60
Db 1 EYTLVSSGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPARLEWVAYISSGSGTTY 60

Qy 61 SDSVKGRFTISRDNASKNTLYLQWRSIRAPDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
Db 61 SDSVKGRFTISRDNASKNTLYLQWRSIRSEDSAMVFCTRVKGTYYPDSWGQGTLLTVSS 119

RESULT 13
AD025153
ID AD025153 standard; protein; 274 AA.
XX
AC AD025153;
XX
DT 01-JUL-2004 (first entry)
XX
DE Melanoma cell adhesion molecule binding protein, scFv5.
XX
KM melanoma cell adhesion molecule; MCAM; invasion; metastasis; cancer;
XX metastatic; sarcoma; cytostatic; anti-idiotypic.
XX
OS Unidentified.
XX
PN EP1382615-A1.
XX
PD 21-JAN-2004.
XX
PF 15-JUL-2002; 2002EP-00015591.
XX
PR 15-JUL-2002; 2002EP-00015591.
XX
PA (XERI-) XERION PHARM AG.
XX
PI Unger CM, Zehetmeyer C;
XX
DR WPI; 2004-101663/11.
XX
DR N-PDB; AD025162.
XX
PT Novel polypeptide useful for detecting melanoma cell adhesion molecules,
PT for treating or preventing metastasis in patient.
XX
PS Claim 1; SEQ ID NO 5; 63pp; English.
XX
CC The invention relates to a novel polypeptide e.g. an antibody fragment,
CC that binds to melanoma cell adhesion molecules (MCAM), comprising a
CC sequence chosen from fully defined sequences of 276, 277, 278, 274, 275,
CC 281 and 273 amino acids as given in the specification. The invention
CC further comprises: a bioconjugate comprising the melanoma cell adhesion
CC molecule binding protein; a diagnostic kit comprising the protein and/or
CC the bioconjugate and a container; a pharmaceutical composition comprising
CC the protein and/or bioconjugate and a carrier; an isolated nucleic acid
CC molecule encoding the protein; a vector comprising the nucleic acid; a
CC host cell comprising the nucleic acid and vector; use of a molecule
CC inhibiting MCAM function in the manufacture of a medicament for the
CC treatment or prevention of invasion and/or metastasis of naturally
CC occurring cancer cells, where invasiveness and/or metastatic potential of
CC the cancer cells depends on melanoma cell adhesion molecule (MCAM)
CC function; and a method for identifying a protein which binds specifically
CC to the extracellular region of MCAM, where the protein is capable of
CC inhibiting invasiveness of sarcoma cells. The novel protein and
CC compositions have cytostatic activity. The MCAM binding protein and
CC bioconjugate are useful for the detection of MCAM, or for identifying a
CC MCAM inhibiting molecule that specifically binds to human MCAM. The MCAM
CC binding protein and bioconjugate are useful for treating or preventing
CC metastasis in a patient, involves administering the MCAM binding protein
CC and bioconjugate to inhibit MCAM mediated invasiveness and/or metastatic
CC potential. The MCAM inhibiting molecule is useful for inhibiting MCAM

CC function in the manufacture of a medicament for treating or preventing
CC invasion and/or metastasis of naturally occurring cancer cells. The MCM
CC inhibiting molecule inhibits gene expression of MCM, where the molecule
CC is an antisense oligonucleotide, an siRNA or siRNA-like hairpin RNA, or a
CC vector leading to the cellular presence of an siRNA or siRNA-like hairpin
CC RNA. The MCM inhibiting molecule inhibits gene expression of MCM, where
CC the molecule binds to the extracellular region of MCM, more particularly
CC the molecule is chosen from a small chemical compound, an antibody, an
CC antibody fragment, an anti-idiotypic antibody, the MCM binding protein
CC or its biocoujugate. This sequence represents an MCM binding protein of
CC the invention.

XX SQ Sequence 274 AA;

Query Match 80.4%; Score 502; DB 8; Length 274;

Best Local Similarity 79.0%; Pred. No. 3,4e-38;

Matches 94; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLVESGDPVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWNAVYISGGSGTYY 60
DB 1 EVLVESGGGLVPGGSLRLSCAAGFTFSYAMSWVRQAPGKLEWNAVYISGGSGTYY 60
QY 61 SDVKGKFTISRNSKNTLYLQKSLRAEDSAVYFCRIVLGTYYRPSWQGTLLTVSS 119
DB 61 ADSVKGRFTISRNSKNTLYLQKNSLRAEDTAVYVCAKSVLAKYFYDWGQGTLLTVSS 119

RESULT 14

AAE28151
ID AAE28151 standard; protein; 119 AA.

XX AAE28151;

DT 27-DEC-2002 (first entry)

XX Human consensus heavy chain variable domain subgroup III (huIII).

XX Human; interferon alpha; IFNalpha; insulin-dependent diabetes mellitus;

XX autoimmune disease; systemic lupus erythematosus; autoimmune thyroiditis;

XX antibody therapy; immunosuppressive; antiinflammatory; dermatological;

XX 9F3 monoclonal antibody; heavy chain variable domain.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 26..35 /note="Complementarity determining region 1 (CDR1)"

FT Region 50..66 /note="Complementarity determining region 2 (CDR2)"

FT Region 99..106 /note="Complementarity determining region 3 (CDR3)"

FT Region 106

XX WO200266649-A2.

XX 29-AUG-2002.

XX 29-JAN-2002; 2002WO-US002709.

XX 22-FEB-2001; 2001US-0270775P.

XX 09-JAN-2002; 2002US-00044896.

XX (GETH) GENENTECH INC.

XX Chuntarapat A, Kim JK, Presta LG, Stewart T;

XX WPI; 2002-682767/73.

XX New anti-interferon alpha monoclonal antibody, 9F3, useful for treating

XX autoimmune diseases e.g. insulin-dependent diabetes mellitus, systemic

XX lupus erythematosus and autoimmune thyroiditis.

XX Disclosure; Page 98; 100pp; English.

XX The present invention relates to novel anti-interferon alpha (IFNalpha)
XX monoclonal antibody, 9F3 which binds to and neutralises a biological
XX activity of IFN-alpha subtypes. The anti-IFNalpha monoclonal antibodies
XX of the invention are useful for treating autoimmune diseases such as
XX insulin-dependent diabetes mellitus, systemic lupus erythematosus and
XX autoimmune thyroiditis. They are useful as reagents in diagnostic assays
XX for IFN-alpha expression, for the affinity purification of various IFN-
XX alpha subtypes from recombinant cell culture or natural resources and for
XX the detection of IFN-alpha in diagnostic assay methods. Sequences of the
XX invention are also useful in antibody therapy. The present sequence is
XX human consensus heavy chain variable domain subgroup III (huIII)

XX SQ Sequence 119 AA;

Query Match 80.0%; Score 499; DB 5; Length 119;

Best Local Similarity 80.7%; Pred. No. 2,6e-38;

Matches 96; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVLVESGDPVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWNAVYISGGSGTYY 60
DB 1 EVLVESGGGLVPGGSLRLSCAAGFTFSYAMSWVRQAPGKLEWNAVYISGGSGTYY 60
QY 61 SDVKGKFTISRNSKNTLYLQKSLRAEDSAVYFCRIVLGTYYRPSWQGTLLTVSS 119
DB 61 ADSVKGRFTISRNSKNTLYLQKNSLRAEDTAVYVCAKRVG--YYDWGQGTLLTVSS 117

RESULT 15

AAE62088
ID AAE62088 standard; protein; 119 AA.

XX AAE62088;

DT 29-MAY-2001 (first entry)

XX Human Vh consensus framework humIII.

XX ErbB2 receptor; anti-ErbB2 antibody; tumour; cancer; breast cancer;

XX leukemia; cytostatic; carcinoma.

XX Homo sapiens.

OS WO200115730-A1.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US023391.

XX 27-AUG-1999; 99US-0151018P.

XX 23-JUN-2000; 2000US-0213822P.

XX (GETH) GENENTECH INC.

XX Baughman SA, Shak S;

XX WPI; 2001-235058/24.

XX Treating a human patient with a disorder characterized by overexpression

XX of ErbB2 receptor such as a tumor or cancer (e.g. metastatic breast

XX carcinoma) comprises administering several dosages of an anti-ErbB2

XX antibody.

XX The invention relates to treating cancer in a human susceptible to or

XX diagnosed with a disorder characterized by overexpression of ErbB2

XX receptor. The method comprises administering an initial dose of at least

XX approx.5 mg/kg of the anti-ErbB2 antibody, and administering subsequent

XX doses of the antibody in approximately the same amount or less than the

XX initial dose. The method is useful for treating a disorder characterized

XX by overexpression of ErbB2 receptor, particularly a benign or malignant

XX tumour, or a cancer. The cancer is selected from breast cancer

CC blocks binding of monoclonal antibody 2C4 to ErbB2 and/or blocks TGF-
CC alpha activation of mitogen-activated protein kinase (MAPK). The present
CC sequence is the consensus framework for the human variable heavy chain.
CC This sequence was used in a sequence alignment homology with the variable
CC heavy chain of antibody 2C4 (see AAB61582)

XX SQ Sequence 119 AA;

Query Match 79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-18;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGGDVFQPGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWAVYISSGGSGTTY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSYAMSVWRQAPGKLEWAVYISDGGSTTY 60
QY 61 SDSVKGRTISRNSKNTLYLQWRSLRAEDSANYFCTRYKLTGYTPDSKQGTLLTVSS 119
DB 61 ADSVKGRFTISRNSKNTLYLQWRSLRAEDTAVYCARGRVGYSLDYWGQGTLLTVSS 119

RESULT 18

AAU74541
ID AAU74541 standard; protein; 119 AA.

XX AC AAU74541;

DT 23-APR-2002 (first entry)

XX DE Human subgroup V_H III heavy chain variable region.

XX Human; subgroup V_H III; ErbB; epidermal growth factor receptor;
XX anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ovary;
XX stomach; endometrium; salivary gland; lung; kidney; colon; colorectum;
XX thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder;
XX glioma; glioblastoma; astrocytic disorder; hypochalamic disorder; antibody;
XX glandular disorder; macrophage disorder; epithelial disorder;
XX stromal disorder; blastocoele disorder; inflammatory disorder;
XX angloenic disorder; immunological disorder; heavy chain variable region.

XX OS Homo sapiens.

XX PN US2002001587-A1.

XX PD 03-JAN-2002.

XX PF 16-MAR-2001; 2001US-00811123.

XX PR 16-MAR-2000; 2000US-0189844P.

XX PR 05-OCT-2000; 2000US-0238327P.

XX PA (ERIC/) ERICKSON S.

XX PA (SCHW/) SCHWALL R.

XX PA (SLIW/) SLIWKOWSKI M.

XX PI Erickson S, Schwall R, Sliwkowski M;

XX DR MPI; 2002-163686/21.

XX PT Treating tumor characterized by overexpression of epidermal growth factor
XX receptor, ErbB or cancer in mammal, comprises administering anti-ErbB
XX antibody-maytansinoid conjugate to the mammal.

XX PS Claim 26; Fig 1; 93pp; English.

XX The invention relates to treating a tumour in a mammal, where the tumour
XX is characterized by the overexpression of an epidermal growth factor
XX receptor (ErbB) and does not respond or responds poorly, to treatment
XX with an anti-ErbB antibody, comprising administering to the mammal an
XX anti-ErbB antibody-maytansinoid conjugate. The method is useful for
XX treating cancer or tumours of the breast, ovary, stomach, endometrium,
XX salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas,
XX prostate and bladder, preferably breast cancer. The breast cancer is a

CC metastatic breast cancer or an aggressive form of metastatic breast
CC cancer which overexpresses ErbB2. The method is also useful for treating
CC neuronal, glial, astrocytic, lymphoma, glioma, glandular, macrophage,
CC epithelial, stromal, blastocoele, inflammatory, angiogenic and
CC immunological disorders. This sequence represents the human subgroup V_H
CC III heavy chain variable region used in the method of the invention

XX SQ Sequence 119 AA;

Query Match 79.8%; Score 498; DB 5; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-18;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGGDVFQPGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWAVYISSGGSGTTY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSYAMSVWRQAPGKLEWAVYISDGGSTTY 60
QY 61 SDSVKGRTISRNSKNTLYLQWRSLRAEDSANYFCTRYKLTGYTPDSKQGTLLTVSS 119
DB 61 ADSVKGRFTISRNSKNTLYLQWRSLRAEDTAVYCARGRVGYSLDYWGQGTLLTVSS 119

RESULT 19

ADE71455
ID ADE71455 standard; protein; 119 AA.

XX AC ADE71455;

DT 29-JAN-2004 (first entry)

XX DE Human antibody variable heavy chain framework.

XX cytochrome; ErbB2 antagonist; tyrosine kinase inhibitor; cancer; ErbB2;
XX ErbB2 antibody; carcinoma; lymphoma; blastoma; sarcoma; liposarcoma;
XX neuroendocrine tumour; mesothelioma; schwannoma; meningioma;
XX adenocarcinoma; melanoma; leukaemia; lymphoid malignancy;
XX squamous cell cancer; epithelial squamous cell cancer; lung cancer;
XX small-cell lung cancer; non-small cell lung cancer;
XX adenocarcinoma of the lung; squamous carcinoma of the lung;
XX cancer of the peritoneum; hepatocellular cancer; gastric cancer;
XX stomach cancer; gastrointestinal cancer; pancreatic cancer; glioblastoma;
XX cervical cancer; ovarian cancer; liver cancer; bladder cancer; hepatoma;
XX breast cancer; colon cancer; rectal cancer; colorectal cancer;
XX endometrial carcinoma; uterine carcinoma; salivary gland carcinoma;
XX kidney cancer; renal cancer; prostate cancer; vulval cancer;
XX thyroid cancer; hepatic carcinoma; anal carcinoma; penile carcinoma;
XX testicular cancer; oesophageal cancer; tumour of the biliary tract;
XX head and neck cancer; human antibody; variable heavy chain framework.

XX OS Homo sapiens.

XX PN US2003086924-A1.

XX PD 08-MAY-2003.

XX PF 10-OCT-2002; 2002US-00268501.

XX PR 25-JUN-1999; 99US-0141316P.

XX PR 23-JUN-2000; 2000US-00602812.

XX PA (GETH) GENENTECH INC.

XX PI Sliwkowski MX;

XX DR MPI; 2004-020226/02.

XX Treating cancer (e.g. carcinoma, lymphoma or sarcoma) that expresses
XX ErbB2 by administering to a patient an anti-ErbB2 antibody, and
XX optionally an epidermal growth factor receptor-targeted drug or a
XX tyrosine kinase inhibitor.

XX Example 3; SEQ ID NO 6; 56pp; English.

CC The invention describes a method of treating cancer that expresses ErbB2
CC comprising administering to a patient an antibody that binds ErbB2.
CC Specifically claimed are antibodies that bind ErbB2, particularly
CC monoclonal antibody 2C4 or humanised 2C4, or monoclonal antibody 4D5 or
CC humanised 4D5. The methods are useful for treating cancer in a patient,
CC particularly a human. The cancer includes carcinoma, lymphoma, blastoma,
CC sarcoma, liposarcoma, neuroendocrine tumour, mesothelioma, schwannoma,
CC meningioma, adenocarcinoma, melanoma, leukaemia, lymphoid malignancy,
CC squamous cell cancer, epithelial squamous cell cancer, lung cancer, small
CC -cell lung cancer, non-small cell lung cancer, adenocarcinoma of the
CC lung, squamous carcinoma of the lung, cancer of the peritoneum,
CC hepatocellular cancer, gastric or stomach cancer, gastrointestinal
CC cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer,
CC liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer,
CC rectal cancer, colorectal cancer, endometrial or uterine carcinoma,
CC salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval
CC carcinoma, thyroid cancer, hepatic carcinoma, anal carcinoma, penile
CC carcinoma, testicular cancer, esophageal cancer, a tumour of the biliary
CC tract, or head and neck cancer. This is the amino acid sequence of human
CC antibody variable heavy chain framework that was used to produce a
CC humanised antibody.

XX SQ Sequence 119 AA;

Query Match 79.8%; Score 498; DB 8; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVSGGDPFVPGGSLRVSCAAGPAPFSGHYMSWVROAPGKLEWAVAYISGGSGTTY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTSSYMSWVROAPGKLEWAVAYISGDGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLTGTYYPDSWCGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGRVGSIVDYWGQGTLLTVSS 119

RESULT 20
ADJ88009

ID ADJ88009 standard; protein; 119 AA.

XX AC ADJ88009;

XX DT 06-MAY-2004 (first entry)

XX DE Human variable heavy chain consensus peptide.

XX KM Cancer; ErbB2; gene therapy; human.

XX OS Homo sapiens.
XX OS unidentified.

XX PN US2004013667-A1.

XX PD 22-JAN-2004.

XX PF 27-JUN-2003; 2003US-00608626.

XX PR 25-JUN-1999; 99US-0141316P.

XX PR 23-JUN-2000; 2000US-00602812.

XX PR 10-OCT-2002; 2002US-00268501.

XX PA (GETH) GENENTECH INC.

XX PI Kelsey SM, Sliwkowski MX;

XX DR WPI; 2004-121529/12.

XX PT Treating cancer that expresses ErbB2 e.g., breast, colon, rectal or
XX PT colorectal cancer comprises administering an antibody that binds to ErbB2
XX PT to a patient.

XX PS Example 3; SEQ ID NO 6; 56pp; English.

XX XX The present invention relates to methods for treating cancer such as
CC carcinoma, lymphoma, blastoma, medulloblastoma, retinoblastoma, sarcoma,
CC liposarcoma, synovial cell sarcoma, neuroendocrine tumour, carcinoid
CC tumour, gastrinoma, islet cell cancer, mesothelioma, schwannoma, acoustic
CC neuroma, meningioma, adenocarcinoma, melanoma, leukaemia, lymphoid
CC malignancy, squamous cell cancer, epithelial squamous cell cancer, lung
CC cancer, small-cell lung cancer, non-small cell lung cancer,
CC adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the
CC peritoneum, hepatocellular cancer, gastric or stomach cancer,
CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
CC cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast
CC cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or
CC uterine carcinoma, salivary gland carcinoma, kidney or renal cancer,
CC prostate cancer, vulvar cancer, thyroid cancer, hepatic carcinoma, anal
CC carcinoma, penile carcinoma, testicular cancer, esophageal cancer, a
CC tumour of the biliary tract or head and neck cancer with anti-ErbB2
CC antibodies. The invention is also useful in gene therapy. The present
CC sequence is human variable heavy chain consensus peptide.

XX SQ Sequence 119 AA;

Query Match 79.8%; Score 498; DB 8; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVSGGDPFVPGGSLRVSCAAGPAPFSGHYMSWVROAPGKLEWAVAYISGGSGTTY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTSSYMSWVROAPGKLEWAVAYISGDGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLTGTYYPDSWCGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGRVGSIVDYWGQGTLLTVSS 119

RESULT 21
ADN12055

ID ADN12055 standard; protein; 119 AA.

XX AC ADN12055;

XX DT 17-JUN-2004 (first entry)

XX DE Variable heavy chain consensus sequence.

XX KM tumor; anti-HER2 antibody; HER2/HER3; HER2/HER1; Cytostatic; cancer.

XX OS Homo sapiens.

XX PN WO2004008099-A2.

XX PD 22-JAN-2004.

XX PF 11-JUL-2003; 2003WO-US021590.

XX PR 15-JUL-2002; 2002US-0396290P.

XX PR 20-JUN-2003; 2003US-0480043P.

XX PA (GETH) GENENTECH INC.

XX PI Koll H, Bossemmaier B, Mueller H, Sliwkowski MX, Kelsey SM;

XX DR WPI; 2004-156546/15.

XX PT Identifying a tumor responsive to treatment with an anti-HER2 antibody,
XX PT useful in treating cancer, comprises detecting the presence of a
XX PT HER2/HER3 and/or HER2/HER1 protein complex.

XX PS Disclosure; SEQ ID NO 6; 105pp; English.

XX CC The present invention relates to identifying a tumor responsive to
XX CC treatment with an anti-HER2 antibody involves detecting the presence of
XX CC an HER2/HER3 and/or HER2/HER1 protein complex in a sample of the tumor.

CC The method is useful in identifying a tumor as responsive to treatment
CC with an anti-HER2 antibody. The methods and antibodies are useful in
CC treating a condition or disorder including tumor or cancer, e.g. breast,
CC prostate, lung, colorectal or ovarian cancer. The present sequence
CC represents a variable heavy chain consensus sequence.

XX Sequence 119 AA;

Query Match 79.8%; Score 498; DB 8; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFSHYAMSVWRQAPGKLEWVAIISGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAIISGGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLTGTYFPDSMCGTLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGRVGSIVDYMGQGLTVTVSS 119

RESULT 22

ADP43329 standard; protein; 119 AA.

ADP43329;

26-AUG-2004 (first entry)

Human monoclonal variable heavy kappa chain antibody SegID 6.

human; variable heavy kappa chain; antibody;
epidermal growth factor receptor; ErbB; ErbB2;
transforming growth factor alpha; benign hyperproliferative disorder;
psoriasis; endometriosis; scleroderma; vascular disease; atherosclerosis;
resenosis; colon polyps; fibroadenoma; respiratory disease;
chronic bronchitis; cystic fibrosis; cytostatic; antipsoriatic;
gynaecological; dermatological; vasotrophic; antiarteriosclerotic;
cardiac; antineural; antilipemic; hypotensive; antiaesthetic;
antiallergic; antiinflammatory; antitussive.

XX Homo sapiens.

XX WO2004048525-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037367.

XX 21-NOV-2002; 2002US-0428027P.

XX (GETT) GENENTECH INC.

XX Sliwkowski MX, Brunetta PG;

XX WPI; 2004-450361/42.

XX Treating non-malignant disease or disorder such as psoriasis,
PT endometriosis, involving abnormal activation or production of epidermal
PT growth factor receptor or ErbB ligand by administering antibody that
PT binds ErbB2 to mammal.

XX Example 3; SEQ ID NO 6; 74pp; English.

XX This invention refers to a novel method for treating a non-malignant
CC disease that involves abnormal activation or production of an epidermal
CC growth factor receptor (ErbB) receptor or an ErbB ligand. Specifically,
CC it refers to the use of humanised murine anti-ErbB2 antibodies to block
CC ligand activation of the ErbB receptor, where the ErbB ligand is a
CC transforming growth factor alpha that promotes mitogen-activated protein
CC kinase (MAPK). The present invention describes conjugating the monoclonal
CC murine antibody 2C4, or more particularly the humanised antibody 574, to
CC a cytotoxic or therapeutic agent such that it can be used to treat a

CC benign hyperproliferative disorder, psoriasis, endometriosis,
CC scleroderma, vascular disease (such as atherosclerosis or resenosis),
CC colon polyps, fibroadenoma or respiratory disease (such as chronic
CC bronchitis or cystic fibrosis). Accordingly, they exhibit cytostatic,
CC antipsoriatic, gynaecological, dermatological, vasotropic, hypotensive,
CC antiarteriosclerotic, cardiac, antineural, antilipemic, hypotensive,
CC antiaesthetic, antiallergic, antiinflammatory and antitussive activities.
CC This polypeptide sequence is the human variable heavy kappa chain protein
CC used to humanise the murine anti-ErbB2 proteins of the invention.

XX Sequence 119 AA;

Query Match 79.8%; Score 498; DB 8; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFSHYAMSVWRQAPGKLEWVAIISGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAIISDDGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLTGTYFPDSMCGTLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGRVGSIVDYMGQGLTVTVSS 119

RESULT 23

ABR01511 standard; protein; 224 AA.

ABR01511;

16-APR-2003 (first entry)

Human anti-TIMP-1 antibody heavy chain #9.

human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLDLR3;
matrix metalloproteinase; MMP; variable heavy chain; VHCOR3; hepatotropic;
variable light chain; cytoskeletal; nephrotropic; cardiac; liver fibrosis;
alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
lupus nephritis; glomerulosclerotic renal disease; lung cancer;
idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

XX Homo sapiens.

XX WO200286085-A2.

XX 31-OCT-2002.

XX 24-APR-2002; 2002WO-US012801.

XX 24-APR-2001; 2001US-0285683P.

XX (PARB) BAYER CORP.

XX (MORP-) MORPHOSYS AG.

XX Pan C, Knorr AM, Schauer M, Hirsch-Dietrich C, Kraft S, Krebs B;

XX WPI; 2003-129114/12.

XX N-PSDB; ABZ74762.

XX New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1) antibodies,
PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
PT cancer.

XX Claim 20; Page 153-154; 228pp; English.

XX The invention relates to a novel purified preparation of a human
CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of TIMP
CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
CC variable light chain (VLC)DR3 region. An antibody preparation of the
CC invention has hepatotropic, cytoskeletal, nephrotropic and cardiac

CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
 CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
 CC fibrosis, benign prostatic hypertrophy, lung cancer or colon cancer. The
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
 CC sequences shown in ABR01502-ABR01545 represent the heavy chain regions of
 CC a human anti-TIMP-1 antibody of the invention
 XX
 SQ Sequence 224 AA;
 Query Match 79.1%; Score 493.5; DB 6; Length 224;
 Best Local Similarity 79.5%; Pred. No. 1.7e-37;
 Matches 97; Conservative 7; Mismatches 13; Indels 5; Gaps 2;
 QY 1 EVQLVSSGGDFVPGGSLRVSCAASGFAFSHYMSWVRQAPGKGLEWVAIYSSGSGSTYY 60
 DB 1 QVQLVSSGGGLVPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVAISGSGSTYY 60
 QY 61 SDSVKGRTISRDNSTNTLYLQNRSLRAEDSAVYFCTRVKLGTY--FDSWCGQTLLVY 117
 DB 61 ADSVKGRTISRDNSTNTLYLQNRSLRAEDTAVYCAR--LDITYPDLPFWCGQTLVTV 118
 QY 118 SS 119
 DB 119 SS 120
 RESULT 24
 ADA89891
 ID ADA89891 standard; protein; 126 AA.
 XX
 AC ADA89891;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE MS-Roche #7 VH region amino acid sequence SEQ ID NO:6.
 XX
 KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
 KW neurotrophic; antiparkinsonian; gene therapy; amyloidogenesis;
 KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
 KW Alzheimer's disease; motor neuropathy; Down's syndrome;
 KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
 KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
 KW neuronal disorder; aging.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS
 PN WO2003070760-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-FEB-2003; 2003WO-EP001759.
 XX
 PR 20-FEB-2002; 2002EP-00003844.
 XX
 PA (HOF) HOFMANN LA ROCHE & CO AG F.
 PA (MORP-) MORPHOSIS AG.
 PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;
 PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
 DR WPI; 2003-663848/62.
 XX
 PT New antibody molecule capable of specifically recognizing two regions of
 PT the beta-A4 peptide, useful for diagnosing, preventing or treating
 PT diseases associated with amyloidogenesis or amyloid-plaque formation
 PT (e.g. dementia).
 XX
 PS Claim 4; Page 39; 312pp; English.

XX The present invention describes an antibody molecule (1) capable of
 CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
 CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
 CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
 CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
 CC cell comprising the vector of (2); (4) preparing (1), comprising
 CC culturing the host cell of (3) under conditions that allow synthesis of
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1)
 CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
 CC (1); (8) testing the resulting Fab optimisation library by panning
 CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
 CC of selected, optimised clones; (11) preparing a pharmaceutical
 CC composition, comprising optimisation of (1), and formulating the
 CC optimised antibody/antibody molecule with a carrier; and (12) a
 CC pharmaceutical composition prepared by method (6). (1) has
 CC neuroprotective, neurotropic and antiparkinsonian activities, and can be
 CC used in gene therapy. The antibody molecule (1), nucleic acid molecule,
 CC vector or host is useful in preparing a pharmaceutical composition for
 CC the prevention and/or treatment of a disease associated with
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
 CC may also be used in preparing a diagnostic composition for the detection
 CC of the disease mentioned above. The antibody is used for the
 CC disintegration of beta-amyloid plaques or for passive immunisation
 CC against beta-amyloid plaque formation. In particular, the disease is
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 126 AA;
 Query Match 78.9%; Score 492.5; DB 6; Length 126;
 Best Local Similarity 76.2%; Pred. No. 1.1e-37;
 Matches 96; Conservative 8; Mismatches 15; Indels 7; Gaps 1;
 QY 1 EVQLVSSGGDFVPGGSLRVSCAASGFAFSHYMSWVRQAPGKLEWVAIYSSGSGSTYY 60
 DB 1 QVQLVSSGGGLVPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVAISGSGSTYY 60
 QY 61 SDSVKGRTISRDNSTNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFDSWCGQT 113
 DB 61 ADSVKGRTISRDNSTNTLYLQNRSLRAEDTAVYCARKGKNTHKPYGYRYFDPWCGQT 120
 QY 114 LFTVSS 119
 DB 121 LFTVSS 126
 RESULT 25
 ADO36357
 ID ADO36357 standard; protein; 119 AA.
 XX
 AC ADO36357;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Intracellular interaction-related scFv protein SeqID21.
 XX
 KW immunoglobulin single domain; intracellular environment;
 KW intracellular interaction; immunoglobulin domain; scFv;
 KW single chain variable fragment.
 XX
 OS Unidentified.
 OS
 PN WO2004046185-A2.
 XX
 PS 03-JUN-2004.
 XX

```

PF 14-NOV-2003; 2003WO-GB004942.
XX
PR 15-NOV-2002; 2002GB-00026729.
XX
PA (MED1-) MEDICAL RES COUNCIL.
XX
PI Rabbits TH, Tanaka T;
XX
DR WPI; 2004-431946/40.
XX
PT Determining the ability of an immunoglobulin single domain to bind to a
PT target in an intracellular environment by assessing the intracellular
PT interaction between the immunoglobulin domain and the target by
PT monitoring the signal.
XX
PS Disclosure; SEQ ID NO 21; 66pp; English.
XX
CC This invention relates to a novel method of determining the ability of an
CC immunoglobulin single domain to bind to a target in an intracellular
CC environment comprising assessing the intracellular interaction between
CC the immunoglobulin domain and the target by monitoring the signal. The
CC method comprises providing a first molecule and a second molecule, where
CC stable interaction of the first and second molecules leads to the
CC generation of a signal; providing a single intracellular immunoglobulin
CC domain which is associated with the first molecule, where the single
CC immunoglobulin domain is free of complementary immunoglobulin domains;
CC providing an intracellular target which is associated with the second
CC molecule, such that association of the immunoglobulin domain and the
CC target leads to stable interaction of the first and second molecules and
CC generation of the signal; and assessing the intracellular interaction
CC between the immunoglobulin domain and the target by monitoring the
CC signal. The methods are useful for determining the ability of an
CC immunoglobulin single domain to bind to a target in an intracellular
CC environment. The present sequence is that of a single chain variable
CC fragment (scFv) protein which was used to illustrate the method of the
CC invention.
XX
SQ Sequence 119 AA;
XX
Query Match 78.8%; Score 492; DB 8; Length 119;
Best Local Similarity 78.2%; Pred. No. 1,2e-37;
Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 EVQLVESGGDFAVQPGSGSLRVSCAASGFAFSHYAMSWVRQAPGKGLIEWAYISSGGSGTTY 60
Dy 1 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
Dy 1 QVQLVESGGGLVQPGGSLRLTCAASGFFSSGGMHWVRQAPGKGLIEWAYAFIRNDSSNEY 60
QY 61 SDSYKGRFTTIRSDNSKNTLYIQMKSIRAEDESNVYFCTYVKLTGYTFPDSWGQGITLTYS 119
Dy 61 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 119
Dy 61 VDSYKGRFTTIRSDNSKNTLYIQMNSIRAEDEVYVYCARGRSRWYFDYWGQGITLTWYSS 119
DB
RESULT 26
ADQ75230
ID ADQ75230 standard; protein; 119 AA.
XX
XX ADQ75230;
XX
DT 09-SEP-2004 (first entry)
DE Immunoglobulin heavy chain variable domain A28 sequence.
XX
XX Immunoglobulin; variable domain.
XX
XX Unidentified.
XX
XX WO2004046189-A2.
XX
XX 03-JUN-2004.
XX
XX 14-NOV-2003; 2003WO-GB004964.
XX
XX 15-NOV-2002; 2002GB-00026731.
XX

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```

PA (MED1-) MEDICAL RES COUNCIL.
XX
PI Rabbits TH, Chung G, Tanaka T, Lobato-Caballero MN, Forster A;
XX
XX WPI; 2004-431950/40.
XX
XX
XX Preparing a double stranded nucleic acid comprises providing a set of
XX three or more overlapping oligonucleotides which anneal to form the + and
XX - strands of a nucleic acid that encodes at least part of an
XX immunoglobulin variable domain.
XX
XX Disclosure; SEQ ID NO 21; 53pp; English.
XX
XX The invention relates to a method of preparing a double stranded nucleic
XX acid, which encodes an immunoglobulin comprising providing a set of three
XX or more overlapping oligonucleotides which anneal to form the + and -
XX strands of a nucleic acid that encodes at least part of an immunoglobulin
XX variable domain. The methods are useful for preparing nucleic acids,
XX preferably immunoglobulin genes. This sequence represents one of the
XX immunoglobulin variable heavy chain produced by the method of the
XX invention.
XX
XX Sequence 119 AA:
XX
XX
XX Query Match 78.8%; Score 492; DB 8; Length 119;
XX Best Local Similarity 78.2%; Pred. No. 1.2e-37;
XX Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
XX
XX 1 EVOLVESGGDPVPGGSGLRVSCAASGFAFHSYMSWRQAPGKGLIEWAYISSGGSGTYY 60
XX 1 QVQLVSGGGLVQPGSSRLRSCAASGFTFSYGMHWRAQPGKLEWYAFTRDQSNERY 60
XX
XX 61 SDSYKGRFTISRDSKNTLYLQMKSLRAEDSAVYFCRTVKLGITYYFDSWGQGLTVSS 119
XX 61 VDSYKGRFTISRDSKNTLYLQNMSLRAEDPAVYVCARGRRSWYIFDVGQGLTVSS 119
XX
XX
XX RESULT 27
XX ADL91330
XX ID ADL91330 standard; protein; 121 AA.
XX
XX ADL91330;
XX
XX 20-MAY-2004 (first entry)
XX
XX VH chain clone A28 of an intracellularly binding immunoglobulin Segid 21.
XX
XX antibody; variable chain; cytosatic; cytoplasmic degradation;
XX intracellular relocation; specific antigen positive cancer; leukaemia;
XX lymphoma; intracellularly binding immunoglobulin; BCR-ABL.
XX
XX Unidentified.
XX
XX WO2003077945-A1.
XX
XX 25-SEP-2003.
XX
XX 14-MAR-2003; 2003WO-GB001077.
XX
XX 14-MAR-2002; 2002GB-00006043.
XX 15-NOV-2002; 2002GB-00026723.
XX 15-NOV-2002; 2002GB-00026727.
XX
XX (MED1-) MEDICAL RES COUNCIL.
XX
XX Lobato-Caballero MN, Rabbits TH;
XX
XX WPI; 2003-779088/73.
XX
XX Use of an intracellularly binding immunoglobulin comprising at least one
XX antibody variable chain, in preparing a medicament for degrading one or
XX more specific antigens, or for treating specific antigen positive cancer,
XX

```

PT e.g. leukemia.
 XX
 PS
 XX Example 1; SEQ ID NO 21; 86pp; English.
 CC This invention relates to novel immunoglobulin molecules that comprise at
 CC least one antibody variable chain VH or VL framework region and are
 CC capable of binding to a specific antigen within an intracellular
 CC environment. Specifically, it refers to antibodies that can form an
 CC insoluble complex with a cognate antigen, such that it can then be target
 CC for degradation via the lysosome or proteasome systems. The present
 CC invention describes the specific target antigen as the oncogenic fusion
 CC protein BCR-ABL or the p53 antigen, such that this method can be used to
 CC prepare a cytostatic medicament for the cytoplasmic degradation or
 CC intracellular relocation of such an antigen or for the treatment of the
 CC specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore,
 CC the immunoglobulins may also be used for therapeutic, prophylactic or
 CC diagnostic applications both in vitro and in vivo, as well as for assay
 CC and reagent applications or in functional genomics. This polypeptide
 CC sequence is a variable heavy chain (VH) framework region of an
 CC intracellularly binding anti-ABL antibody of the invention.
 CC
 XX Sequence 121 AA;
 SQ
 Query Match 78.8%; Score 492; DB 7; Length 121;
 Best Local Similarity 78.2%; Pred. No. 1.2e-37;
 Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 QY 1 EVOLVSSGGDFVOPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
 Db 3 QVOLVSSGGGLVOPGSLRVSCAASGFTSSYGMHWVRQAPGKLEWVAIRDGSNEY 62
 QY 61 SDSVKGRFTISRDNKNITLYLQWRSLRAEDSAVYFCTRVGLGTYFDSWGQGLTVTSS 119
 Db 63 VDSVKGRFTISRDNKNITLYLQWNSLRADPTAVYYCARGRSMYTFDYGQGLTVTSS 121
 RESULT 28
 AAUI4320
 ID AAUI4320 standard; protein; 313 AA.
 XX
 AC AAUI4320;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human novel protein #191.
 XX
 XX Human: novel protein; Antianaemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cycostatic; neuroprotective; vulnerary; noctropic;
 KW anticovulsaent; antiarthritic; cerebroprotective; antifungal; antivital;
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO200155437-A2.
 PN
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US002623.
 XX
 PR 25-JAN-2000; 2000US-00491404.
 XX
 PA (HYSR-) HYSR INC.
 XX
 PI Tang YT, Liu C, Dymnac RT,
 XX
 DR WPI; 2001-451939/48.
 XX
 DR N-PDB; AAS22625.
 XX
 PT Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage.

XX
 XX Example 4; Page 630-631; 894pp; English.
 PS
 XX
 CC The invention relates to polynucleotides encoding novel human proteins or
 CC their active domains. The polypeptides, polynucleotides and antibodies
 CC raised against the polypeptides are used in a method of treatment of a
 CC mammal and prevention of disorders caused by the aberrant protein
 CC expression or activity. The polypeptides can be used as molecular weight
 CC markers, food supplements, and in antibody production. The polypeptides
 CC are used to identify compounds which bind to the polypeptides.
 CC Polynucleotides of the invention are used as probes and primers, for
 CC sequencing, for chromosome or gene mapping, in the production of
 CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
 CC therapy. Polypeptides of the invention can be used to target drugs to a
 CC tumour, in assays to determine biological activity, to raise
 CC antibodies/elicite an immune response, to determine quantitative protein
 CC levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
 CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
 CC diseases, nervous system disorders, and infection. The present sequence
 CC represents a protein of the invention
 CC
 XX Sequence 313 AA;
 SQ
 Query Match 78.8%; Score 492; DB 4; Length 313;
 Best Local Similarity 74.8%; Pred. No. 3.2e-37;
 Matches 95; Conservative 9; Mismatches 15; Indels 8; Gaps 1;
 QY 1 EVOLVSSGGDFVOPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
 Db 61 EVOLVSSGGGLVOPGSLRVSCAASGFTSSYAMSWVRQAPGKLEWVAIYSSGSGSTYY 120
 QY 61 SDSVKGRFTISRDNKNITLYLQWRSLRAEDSAVYFCTRVGLG-----TYFDSWGQGL 112
 Db 121 ADSVKGRFTISRDNKNITLYLQWNSLRADPTAVYYCARGRSMYTFDYGQGLTVTSS 180
 QY 113 TLTVTSS 119
 Db 181 TLTVTSS 187
 RESULT 29
 ADI58099
 ID ADI58099 standard; protein; 251 AA.
 XX
 AC ADI58099;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Reg IV-specific single chain antibody fragment (scFv) #58.
 XX
 XX antibody, regeneration IV; Reg IV; single chain antibody fragment; scFv;
 KW inflammatory bowel disorder; ulcerative colitis; Crohn's disease;
 KW diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
 KW cancer; human.
 XX
 XX Homo sapiens.
 OS
 XX WO2004003144-A2.
 PN
 XX
 PD 08-JAN-2004.
 XX
 PF 26-JUN-2003; 2003WO-US019908.
 XX
 PR 01-JUL-2002; 2002US-0392382P.
 XX

CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
 CC Ser-Gly-Tyr ADA8986 or its fragment, and the second region comprises the
 CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-
 CC Gly ADA8987 or its fragment. Also described: (1) a nucleic acid molecule
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
 CC cell comprising the vector of (2); (4) preparing (1), comprising
 CC culturing the host cell of (3) under conditions that allow synthesis of
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1)
 CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
 CC (1); (8) testing the resulting Fab optimisation library by panning
 CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
 CC of selected, optimised clones; (11) preparing a pharmaceutical
 CC composition, comprising optimisation of (1), and formulating the
 CC pharmaceutical composition prepared by method (8). (1) has
 CC neuroprotective, neurotropic and antiparkinsonian activities, and can be
 CC used in gene therapy. The antibody molecule (1), nucleic acid molecule,
 CC vector or host is useful in preparing a pharmaceutical composition for
 CC the prevention and/or treatment of a disease associated with
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
 CC may also be used in preparing a diagnostic composition for the detection
 CC of the disease mentioned above. The antibody is used for the
 CC differentiation of beta-amyloid plaques or for passive immunisation
 CC against beta-amyloid plaque formation. In particular, the disease is
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
 CC present sequence is used in the exemplification of the present invention.

XX Sequence 126 AA;

SO Query Match 78.4%; Score 489.5; DB 6; Length 126;

Best Local Similarity 75.4%; Pred. No.2.1e-37; Mismatches 13; Indels 7; Gaps 1;

Matches 99; Conservative 11; Mismatches 13; Indels 7; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFASHYMSWVRQAPGKLEWVAYISSGSGTYY 60
 DB 1 QVQLVDSGGGVQPGGSLRVSCAAGFAFASHYMSWVRQAPGKLEWVAYISSGSGTYY 60
 QY 61 SDSVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFPSKQGT 113
 DB 61 ADSVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFPSKQGT 120
 QY 114 LVTYSS 119
 DB 121 LVTYSS 126

RESULT 32
 AAR95216
 ID AAR95216 standard; protein; 119 AA.

XX AAR95216;
 AC 16-DEC-1996 (first entry)

XX Human foetal immunoglobulin 56p1'CL variable heavy chain.

XX Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;
 KM detection; imaging; immunotoxin; targeting; assay; immunoassay;
 XX Lewis(Y) carbohydrate antigen.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 31..35

FT Domain /label= CDR 1.

FT Domain 50..66

FT Domain /label= CDR 2.

FT Domain 99..108

FT /label= CDR 3.

XX MO9613594-A1.

XX 09-MAY-1996.

XX 26-OCT-1995; 95WO-US013811.

XX 28-OCT-1994; 94US-00331396.

XX 28-OCT-1994; 94US-00331397.

XX 28-OCT-1994; 94US-00331398.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M,
 PI Fitzgerald D, Brinkmann U, Pal L,
 XX WPI, 1996-251462/25.

XX Single chain fusion proteins and antibodies - useful to diagnose and
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.

XX Example 13; Fig 11A; 116pp; English.

XX A novel recombinant DNA molecule which encodes a single chain fusion
 CC protein or antibody comprising the Fv region of both the light and heavy
 CC chains of an antibody (Ab) fused together, and an effector molecule,
 CC where the fusion protein or Ab has the binding specificity of monoclonal
 CC Ab (MAb) B1, B3 or B5, can be used for the production of such fusion
 CC proteins or antibodies. The fusion proteins can be used in compositions
 CC as an immunotoxin to inhibit tumour cell growth. The single chain
 CC antibody can be used to detect the presence or absence of cells bearing a
 CC Lewis(Y) carbohydrate antigen in a patient. The antibodies are also
 CC useful as multiple targeting moieties, providing at least 2 kinds of
 CC biological activity. They can also be used in diagnostic assays and for
 CC the imaging of tumours when attached to a radiolabel and for the
 CC pathological diagnosis of tumours. Humanised antibodies are less
 CC immunogenic than the mouse MAbs B1, B3 and B5, making them more suitable
 CC for long term treatment

SO Sequence 119 AA;

Query Match 78.4%; Score 489; DB 2; Length 119;

Best Local Similarity 79.0%; Pred. No.2.2e-37; Mismatches 18; Indels 0; Gaps 0;

Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFASHYMSWVRQAPGKLEWVAYISSGSGTYY 60
 DB 1 QVQLVDSGGGVQPGGSLRVSCAAGFAFASHYMSWVRQAPGKLEWVAYISSGSGTYY 60
 QY 61 SDSVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY--YFDSWGQGTLLTVSS 119
 DB 61 ADSVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY--YFDSWGQGTLLTVSS 119

RESULT 33
 ADA43059
 ID ADA43059 standard; protein; 143 AA.

XX ADA43059;

XX 20-NOV-2003 (first entry)

XX Human antibody HD4 heavy chain protein.

XX cytotoxic; immunosuppressive; anti-allergic; human leukocyte antigen;
 KM HLA-DR; antibody; hybridoma; diagnosis; cancer; allergy; sarcoma;
 KM myeloma; lymphoma; leukaemia.

XX Homo sapiens.

XX NO2003033538-A1.

XX

XX

PD 24-APR-2003.
 XX
 XX 15-OCT-2002; 2002MO-JP010665.
 PF
 XX
 PR 15-OCT-2001; 2001JP-00317054.
 XX
 XX (KIRI) KIRIN BEER KK.
 PA
 PI Tawara T, Kataoka S;
 XX
 XX WPI: 2003-403196/38.
 DR N-PSDB; ADA43205.
 XX
 PT HLA-DR binding antibodies useful as immunosuppressant agents for
 PT treatment and prevention of cancer and allergies.
 XX
 PS Claim 57; Page 40; 147pp; Japanese.
 XX
 XX The invention relates to novel human leukocyte antigen DR (HLA-DR)
 CC binding antibodies and their functional fragments and soluble domains.
 CC The specification also includes: a) hybridomas producing the antibodies;
 CC b) nucleic acids encoding all or part of the antibodies; c) expression
 CC vectors containing the nucleic acids; d) hosts transformed by the vectors
 CC ; e) method for preparation of the antibodies by culture of the
 CC transformed hosts; and f) agents for the prevention, treatment and
 CC diagnosis of cancer and allergies, containing the antibodies. The
 CC antibodies are used in the prevention, treatment and diagnosis of
 CC allergies and of cancers including breast, colon, kidney, stomach, ovary,
 CC pancreas, uterus, oesophagus, liver, skin, bladder and vascular cancer,
 CC sarcoma, myeloma, lymphoma (including T-cell lymphoma, Hodgkin's lymphoma
 CC and non-Hodgkin's lymphoma) and leukaemia (including chronic and acute
 CC lymphocytic leukaemia). This sequence represents the heavy chain of the
 CC HD4 antibody targeted to the HLA-DR chains.
 XX
 SQ Sequence 143 AA;
 Query Match 78.4%; Score 489; DB 6; Length 143;
 Best Local Similarity 78.0%; Pred. No. 2,7e-37;
 Matches 96; Conservative 9; Mismatches 14; Indels 4; Gaps 2;
 QY 1 EVQLVSGGDFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKGLEWVAIISGGSGTTY 60
 DB 20 EVQLSSGGGLVPGGSLRLSCAAGFTFSSYAMTWVRQAPGKGLEWVSGISGGSGTTY 79
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYK-LGTY--PDSWGQGLTVSS 116
 DB 80 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARHDSGSYFYWPDYWGQGLTVT 139
 QY 117 VSS 119
 DB 140 VSS 142
 RESULT 34
 AAY15124
 ID AAY15124 standard; protein; 240 AA.
 AC AAY15124;
 DT 07-FEB-2000 (first entry)
 DE Anti-human CTLA-4 sfv.
 DE Anti-human CTLA-4 sfv.
 KW Anti-human CTLA-4 sfv; single chain antibody; phage; human CTLA-4;
 KW membrane-associated protein; ligand; activated T-cell; B7; CD28;
 KW co-stimulatory signal; T-cell proliferation; xenograft; organ transplant;
 KW xenograft-specific immunosuppression.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 116..130
 FT Region /label= linker_region

XX
 PN WO957266-A2.
 XX
 XX 11-NOV-1999.
 PD
 XX
 PF 30-APR-1999; 99MO-GB001350.
 XX
 XX 30-APR-1998; 98GB-00009280.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 PI Lechler IR, Dörling A;
 XX
 XX WPI: 2000-038815/03.
 DR N-PSDB; AA228996.
 XX
 PT Inhibiting T-cell mediated rejection of xenotransplanted organs.
 XX
 PS Claim 9; Fig 9; 43pp; English.
 XX
 XX The present sequence is the anti-human CTLA-4 sfv. This is a membrane -
 CC associated protein which binds to CTLA-4. The single chain antibody (sfv)
 CC from a phage displays differential binding to human CTLA-4 -Ig protein
 CC which is the recipient organism. The anti-CTLA4 sfv functions as a
 CC ligand binding to CTLA-4 on activated T-cells and antagonises the co-
 CC stimulatory signal provided by the interaction between donor B7 and
 CC recipient CD28. Cells expressing the anti-CTLA4 sfv failed to stimulate
 CC T-cell proliferation. This is used in xenograft-specific
 CC immunosuppression
 XX
 SQ Sequence 240 AA;
 Query Match 78.4%; Score 489; DB 3; Length 240;
 Best Local Similarity 79.8%; Pred. No. 4,6e-37;
 Matches 95; Conservative 6; Mismatches 16; Indels 2; Gaps 1;
 QY 1 EVQLVSGGDFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKGLEWVAIISGGSGTTY 60
 DB 1 EVQLVSGGGLVPGGSLRLSCAAGFTFSSYAMSWVRQAPGKGLEWVAIISGGSGTTY 60
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYK-LGTY--PDSWGQGLTVSS 119
 DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARA--GRILPDYWGQGLTVVSS 117
 RESULT 35
 AAY15125
 ID AAY15125 standard; protein; 240 AA.
 AC AAY15125;
 DT 07-FEB-2000 (first entry)
 DE Anti-murine CTLA-4 M1 sfv.
 DE Anti-murine CTLA-4 M1 sfv.
 KW Anti-murine CTLA-4 sfv; M1 sfv; single chain antibody; murine CTLA4;
 KW membrane-associated protein; chimeric construct; extracellular domain;
 KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;
 KW recipient CD28; T-cell proliferation;
 KW xenograft-specific immunosuppression.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX WO957266-A2.
 PN
 XX 11-NOV-1999.
 PD
 XX
 PF 30-APR-1999; 99MO-GB001350.
 XX
 XX 30-APR-1998; 98GB-00009280.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Lechler IR, Dorling A;
PI WPI; 2000-038815/03.
XX N-PSDB; AAZ28997.
DR
XX Inhibiting T-cell mediated rejection of xenotransplanted organs.
PT Claim 9; Fig 11; 43pp; English.
XX
XX The present sequence is anti-murine CTLA-4 sFv (M1 sFv). This is a
CC membrane-associated protein which binds to CTLA-4. Chimeric constructs
CC comprising DNA sequences encoding the extracellular domain of murine
CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.
CC The anti-CTLA4 sFv functions as a ligand binding to CTLA-4 on activated
CC T-cells and antagonises the co-stimulatory signal provided by the
CC interaction between donor B7 and recipient CD28. Cells expressing the
CC anti-CTLA4 sFv failed to stimulate T-cell proliferation. This is used in
CC xenograft-specific immunosuppression
XX
SQ Sequence 240 AA;
Query Match 78.4%; Score 489; DB 3; Length 240;
Best Local Similarity 79.8%; Pred. No. 4.6e-37; Mismatches 16; Indels 2; Gaps 1;
Matches 95; Conservative 6; Mismatches 16; Indels 2; Gaps 1;
QY 1 EVQLVSGDYPVPGGSLRVSQAAGFAFSGHYAMSVWRQAPGKLEWVAIYSSGSGSTYY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAAGFTFSYAMSVWRQAPGKLEWVAISGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQKRSIPAEPSAVYFCTRVLAGTYYPDSWGGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQKNSLRAPEDTAVYYCARA--GRILFDYWGQGTLLTVSS 117
QY
DB
RESULT 36
ADIS8058
ID ADIS8058 standard; protein; 248 AA.
XX
AC ADIS8058;
XX
XX 22-APR-2004 (first entry)
XX
XX Reg IV-specific single chain antibody fragment (scFv) #17.
XX
XX antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv;
XX inflammatory bowel disorder; ulcerative colitis; Crohn's disease;
XX diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
XX cancer; human.
XX
XX Homo sapiens.
XX
XX WO2004003144-A2.
XX
XX 08-JAN-2004.
XX
XX 26-JUN-2003; 2003WO-US019908.
XX
XX 01-JUL-2002; 2002US-0392382P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA;
XX
XX WPI; 2004-071976/07.
XX N-PSDB; ADIS8124.
XX
XX Novel antibody, useful for treating, preventing or ameliorating
PT inflammatory bowel disorder, cancer of the gastrointestinal tract or
PT diabetes (non-insulin dependent diabetes or insulin dependent diabetes).
XX
XX Claim 2; SEQ ID NO 18; 324pp; English.
XX

CC The invention comprises an antibody that specifically binds a
CC regeneration IV (Reg IV) protein. The invention specifically comprises
CC the amino acid and coding sequences of single chain antibody fragments
CC (scFv's) that bind Reg IV protein. The antibody of the invention is
CC useful for treating, preventing and ameliorating inflammatory bowel
CC disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g.
CC non-insulin dependent diabetes or insulin dependent diabetes), and cancer
CC of the gastrointestinal tract. The antibody of the invention is also
CC useful for detecting the expression of a Reg IV protein. The present
CC amino acid sequence represents an scFv of the invention.
XX
SQ Sequence 248 AA;
Query Match 78.4%; Score 489; DB 8; Length 248;
Best Local Similarity 77.7%; Pred. No. 4.8e-37; Mismatches 16; Indels 2; Gaps 1;
Matches 94; Conservative 9; Mismatches 16; Indels 2; Gaps 1;
QY 1 EVQLVSGDYPVPGGSLRVSQAAGFAFSGHYAMSVWRQAPGKLEWVAIYSSGSGSTYY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAAGFTFSYAMSVWRQAPGKLEWVAISGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQKRSIPAEPSAVYFCTRVLAGT--YYPDSWGGTLLTVSS 118
DB 61 ADSVKGRFTISRDNKNTLYLQKNSLRAPEDTAVYYCARSDSDSYYPDSWGGTLLTVSS 120
QY 119 S 119
DB 121 S 121
QY
DB
RESULT 37
ABR01519
ID ABR01519 standard; protein; 220 AA.
XX
XX ABR01519;
XX
XX 16-APR-2003 (first entry)
XX
XX Human anti-TIMP-1 antibody heavy chain #17.
XX
XX Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLDLR3;
XX matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatocrotic;
XX variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;
XX alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
XX lupus nephritis; glomerulonephrotic renal disease; lung cancer;
XX idiopathic pulmonary fibrosis; benign prostatic hypertrophy; colon cancer.
XX
XX Homo sapiens.
XX
XX WO200286085-A2.
XX
XX 31-OCT-2002.
XX
XX 24-APR-2002; 2002WO-US012801.
XX
XX 24-APR-2001; 2001US-0285683P.
XX
XX (PARB) BAYER CORP.
XX (MORP-) MORPHOSYS AG.
XX
XX Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
XX
XX WPI; 2003-129114/12.
XX N-PSDB; ABZ74790.
XX
XX New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,
PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
PT cancer.
XX
XX Claim 20; Page 159-160; 228pp; English.
XX
XX The invention relates to a novel purified preparation of a human
CC

Query Match	78.1%	Score 487.5	DB 2	Length 443
Best Local Similarity	82.4%	Feat. No. 1.2e-36		
Matches	98	Conservative	6	Mismatches 12
				Indels 3
				Gaps 2
Qy	1	EVOLVESGCDLVPQGGSLRVS	CAASGFAFSAFSAWSWVQA	PGKLEWVAVYSSGSGSGTYY 60
Db	1	EVOLVESGCGLVQVQGGSLRLSCA	SGFFSFYSANSWRQAQKGL	EWVASISTGGS-TYY 59
Qy	61	SDSVKGRFTTIRDSKNTLYIQM	SLRAEDSAVYFCTRWKLTGY	YFDSWGCGTLLTVSS 119
Db	60	PDSVKGRTTIRDNKNTLYIQM	SLRAEDTVAVVYCCARDYD	-YFDYWGCGTLLTVSS 116
RESULT 40				
ID	ABB57571	standard; peptide; 121 AA.		
XX	ABB57571			
AC	ABB57571			
XX	ABB57571			
DT	18-MAR-2002	(first entry)		
DE	HLA-DR-specific protein MS-GPIC4 VH sequence.			
XX				
KM	Immunomodulatory human MHC class II antigen-binding protein; HLA;			
KM	human leukocyte antigen; immune system; immunosuppression; antibody;			
KM	major histocompatibility complex; antirheumatic; antiarthritic;			
KM	neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;			
KM	immunosuppressive; dermatological; antihydroid; nephrotropic; psoriasis;			
KM	thrombotic; hepatotropic; immune response suppressor; narcolepsy;			
KM	rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinits;			
KM	grave's disease; insulin-dependent diabetes; Hashimoto's disease;			
KM	systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;			
KM	transplant rejection; graft versus host disease; pemphigus vulgaris;			
KM	glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;			
XX	irritable bowel disease; Sjogren's syndrome.			
XX				
OS	Homo sapiens.			
XX	Synthetic.			
XX				
PN	WO200187338-A1.			
PD	22-NOV-2001.			
XX				
PF	14-MAY-2001; 2001WO-US015626.			
XX				
PR	12-MAY-2000; 2000EP-00110063.			
PR	06-OCT-2000; 2000US-0238762P.			
XX				
PA	(GPCB-) GPC BIOTECH AG.			
PA	(MORP-) MORPHOSYS AG.			
XX				
PI	Nagy Z, Tesar M, Thomassen-Wolf E;			
XX				
RK	WPI; 2002-075389/10.			
XX				
FT	Composition for suppressing immune response, treating diseases of immune			
FT	system, has polypeptide comprising antibody-based antigen-binding domain			
PT	of human composition, which binds antigen expressed on a cell surface.			
XX				
PS	Example; Fig 15; 139pp; English.			
XX				
CC	The present invention describes a composition (I), comprising a			
CC	polypeptide comprising an antibody-based antigen-binding domain of human			
CC	composition with binding specificity for an antigen expressed on the			
CC	surface of a cell, where treating cells expressing the antigen with the			
CC	polypeptides leads to suppression of an immune response, and the IC50 for			
CC	the suppression of immune response is 1 microM or less. (I) has			
CC	antirheumatic, antiarthritic, neuroprotective, antipsoriatic,			
CC	antidiabetic, immunosuppressive, dermatological,			
CC	antithyroid, nephrotropic, thrombotic and hepatotropic activities, and			
CC	can be used as a suppressor of immune response. (I) is useful for			
CC	suppressing activation or proliferation of a cell of the immune system,			
CC	suppressing IL-2 secretion by a cell, the interaction of a cell of the			

immune system with another cell, immunosuppressing a patient and for killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on the surface of the cell, where neither cytotoxic entities nor immunological mechanisms are needed to cause or lead to the killing. (1) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvenile arthritis, multiple sclerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus erythematosus, ankylosing spondylitis, transplant rejection, graft versus host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris, glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. CC ABA924469 to ABA924474 and ABB57457 to ABB57590 represent sequence used in the exemplification of the present invention

Query Match	78.0%	Score 487	DB 5	Length 121
Best Local Similarity	78.5%	Pred. No. 3.4e-37		
Matches	95	Conservative	7	Mismatches 17
			Indels	2
			Gaps	1
QY	1	EVOLVESGDEVFVQGGSLRVSCAASGFAFSHYAMSWRQAPQKGLWVAIYISGGSGTTY	60	
DB	1	EVQLVESGGLAVQGGSLRLSCAASGFFPSFVAMSWVRQAPQKGLWVAISGSGSTFY	60	
QY	61	SDSVKGRFTISRDN SKNTLYIQMSLRAEDEAVYFCTVKLGTYY--YDSSNGCFTLLTVS	118	
		:::	:::	:::
DB	61	ADSVKGRFTISRDN SKNTLYIQMNSLRAEDEAVYVYCARSSPMVGEGLDMLQCGTLTVTS	120	
QY	119	S	119	
DB	121	S	121	

Search completed: December 17, 2004, 18:29:09
Job time : 363.68 secs

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OM protein - protein search, using SW model

Run on: December 17, 2004, 18:13:27 ; Search time 72.2022 Seconds
(without alignments)
109.302 Million cell updates/sec

Title: US-10-089-500-9

Perfect score: 624
Sequence: 1 EVQLVDSGDPVPGGSLRV.....KLGTYYFDSWGQGLTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	92.8	130	4	US-09-225-322B-18
2	579	92.8	130	4	US-09-764-304-18
3	569	91.2	130	4	US-09-225-322B-8
4	569	91.2	130	4	US-09-764-304-8
5	498	79.8	119	4	US-09-648-067A-15
6	495.5	79.4	120	2	US-07-934-373C-4
7	495.5	79.4	120	3	US-08-437-642B-4
8	495.5	79.4	120	4	US-08-146-206C-4
9	495.5	79.4	120	4	US-09-705-686-4
10	495.5	79.4	120	4	US-09-705-392A-4
11	489	78.4	119	1	US-08-331-398A-46
12	489	78.4	119	2	US-08-331-397B-46
13	489	78.4	119	2	US-08-759-804A-46
14	489	78.4	119	3	US-09-227-693-46
15	489	78.4	125	2	US-08-428-197-1
16	489	78.4	125	5	PCT-US93-10555-1
17	487.5	78.1	135	3	US-08-579-378A-20
18	487.5	78.1	135	5	PCT-US96-11152-4
19	485.5	77.8	122	2	US-07-994-373C-21
20	485.5	77.8	122	3	US-08-437-642B-21
21	485.5	77.8	122	4	US-08-146-206C-21
22	485.5	77.8	122	4	US-09-705-686-21
23	485.5	77.8	122	5	PCT-US93-10555-1
24	485.5	77.8	122	5	PCT-US93-10555-1
25	485.5	77.8	263	3	US-09-089-821-3
26	485.5	77.8	263	4	US-09-956-086-3
27	485.5	77.8	263	4	US-09-956-087-3

28	485.5	77.8	283	3	US-09-420-592A-6	Sequence 6, Appl
29	485.5	77.8	283	4	US-09-985-442-6	Sequence 6, Appl
30	485.5	77.8	283	4	US-09-983-580-6	Sequence 6, Appl
31	485	77.7	123	4	US-09-840-459-82	Sequence 82, Appl
32	485	77.7	123	4	US-09-497-625A-82	Sequence 82, Appl
33	483.5	77.5	140	3	US-08-983-607-32	Sequence 32, Appl
34	481	77.1	113	3	US-08-974-899-6	Sequence 6, Appl
35	481	77.1	113	3	US-09-795-798-6	Sequence 6, Appl
36	480.5	77.0	120	3	US-09-025-769B-63	Sequence 63, Appl
37	480.5	77.0	120	3	US-09-025-769B-63	Sequence 63, Appl
38	480.5	77.0	120	4	US-09-490-070A-38	Sequence 38, Appl
39	480.5	77.0	120	4	US-09-490-070A-63	Sequence 63, Appl
40	480.5	77.0	120	4	US-09-490-153-38	Sequence 38, Appl
41	480.5	77.0	120	4	US-09-490-153-63	Sequence 63, Appl
42	480.5	77.0	281	3	US-09-025-769B-178	Sequence 178, App
43	480.5	77.0	281	4	US-09-490-070A-178	Sequence 178, App
44	480.5	77.0	281	4	US-09-490-153-178	Sequence 178, App
45	478.5	76.7	124	4	US-09-840-459-89	Sequence 89, Appl

ALIGNMENTS

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RESULT 1
US-09-225-322B-18
; Sequence 18, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMAWA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA KM-641
US-09-225-322B-18

Query Match          92.8%; Score 579; DB 4; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-49;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVDSGDPVPGGSLRVCAAGFAFHHYMSWVROAPGKLEWVAIYSGSGTYY 60
DB 11 EVQLVDSGDPVPGGSLRVCAAGFAFHHYMSWVROAPGKLEWVAIYSGSGTYY 70

QY 61 SDVSKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRYVLTGYTYSWGQGLTVSS 119
DB 71 SDVSKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRYVLTGYTYSWGQGLTVSS 129

RESULT 2
US-09-764-304-18
; Sequence 18, Application US/09764304
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/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ EARLIER FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 18
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: CDNA KM-641
US-09-764-304-18
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Query Match          92.8%; Score 579; DB 4; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-49;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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Db 11 EYLVESGGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPARLEWAVYISSGSGGTTY 70
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QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVGLGTYFPDSMGOGTLLTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 71 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVGLGTYFPDSMGOGTLLTVSS 129
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RESULT 3
US-09-225-322B-8
/ Sequence 8, Application US/09225322B
/ Patent No. 6437098
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/225,322B
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 8
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/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-8
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Query Match          91.2%; Score 569; DB 4; Length 130;
Best Local Similarity 90.8%; Pred. No. 9.6e-49;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 11 EYLVESGGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPARLEWAVYISSGSGGTTY 70
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVGLGTYFPDSMGOGTLLTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 71 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVGLGTYFPDSMGOGTLLTVSS 129
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RESULT 4
US-09-764-304-8
/ Sequence 8, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
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/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ EARLIER FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 8
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/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: CDNA KM-641
US-09-764-304-8
```

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Query Match          91.2%; Score 569; DB 4; Length 130;
Best Local Similarity 90.8%; Pred. No. 9.6e-49;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 EVLVESGGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPGKGLMWAVYISSGSGGTTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 11 EYLVESGGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPARLEWAVYISSGSGGTTY 70
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVGLGTYFPDSMGOGTLLTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 71 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVGLGTYFPDSMGOGTLLTVSS 129
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 5
US-09-648-067A-15
/ Sequence 15, Application US/09648067A
/ Patent No. 6627196
```

GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
APPLICANT: Shaik Steven
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US/09/648,067A
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: VH consensus sequence
US-09-648-067A-15

Query Match 79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 8,3e-42;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYMSWVRQAPGKLEWVAAYISGGSGTTY 60
DB 1 EVOLVESGGLVPGGSLRVSCAAGFAPSHYMSWVRQAPGKLEWVAAYISGGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGY-YFDSWGCGTLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGY-YFDSWGCGTLTVSS 119

RESULT 6
US-07-934-373C-4
Sequence 4, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-4

Query Match 79.4%; Score 495.5; DB 2; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYMSWVRQAPGKLEWVAAYISGGSGTTY 60
DB 1 EVOLVESGGLVPGGSLRVSCAAGFAPSHYMSWVRQAPGKLEWVAAYISGGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGY-YFDSWGCGTLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGY-YFDSWGCGTLTVSS 120

RESULT 7
US-08-437-642B-4
Sequence 4, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:

APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-4

Query Match 79.4%; Score 495.5; DB 3; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVQPGSLRVSCAASGAFSHYMSWVRQAPGKLEWAVIYSSGGSGTTY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSIDYMSWVRQAPGKLEWAVIYSSGGSDTTY 60
QY 61 SDVSKGRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGQGLTVVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGQGLTVVSS 120

RESULT 8

US-08-146-206C-4
Sequence 4, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-4

Query Match 79.4%; Score 495.5; DB 4; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVQPGSLRVSCAASGAFSHYMSWVRQAPGKLEWAVIYSSGGSGTTY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSIDYMSWVRQAPGKLEWAVIYSSGGSDTTY 60
QY 61 SDVSKGRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGQGLTVVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGQGLTVVSS 120

RESULT 9

US-09-705-686-4
Sequence 4, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-NOV-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-705-686-4
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 79.4%; Score 495.5; DB 4; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVQPGSLRVSCAASGAFSHYMSWVRQAPGKLEWAVIYSSGGSGTTY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSIDYMSWVRQAPGKLEWAVIYSSGGSDTTY 60
QY 61 SDVSKGRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGQGLTVVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGQGLTVVSS 120

RESULT 10

US-09-705-392A-4
Sequence 4, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-NOV-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PDI1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-705-392A-4
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
Query Match 79.4%; Score 495.5; DB 4; Length 120;
Best Local Similarity 80.8%; Pred. No. 1,5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;
Qy 1 EVOLVSGGDFVQPGSLRVSCAAGFAPSHYAMSWVROAPGKLEWVAIYSSGSGTTY 60
Db 1 EVOLVSGGGLVQPGSLRVSCAAGFTFSDYAMSWVROAPGKLEWVAIYSSGSGTTY 60
Qy 61 SDSVKRFTISRNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-YFDSWGCGTLTVSS 119
Db 61 ADSVKRFTISRNSKNTLYLQMRSLRAEDTAIYVCARDRGAVSYFDVWGCGTLTVSS 120
RESULT 11
US-08-331-398A-46
Sequence 46, Application US/08311398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1.C1 Variable Heavy chain (V-H)"
US-08-331-398A-46
Query Match 78.4%; Score 489; DB 1; Length 119;
Best Local Similarity 79.0%; Pred. No. 6,4e-41;
Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
Qy 1 EVOLVSGGDFVQPGSLRVSCAAGFAPSHYAMSWVROAPGKLEWVAIYSSGSGTTY 60
Db 1 QVELVSGGGLVQPGSLRVSCAAGFTFSDYAMSWVROAPGKLEWVAIYSSGSGTTY 60
Qy 61 SDSVKRFTISRNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-YFDSWGCGTLTVSS 119
Db 61 ADSVKRFTISRNSKNTLYLQMRSLRAEDTAIYVCARDRGAVSYFDVWGCGTLTVSS 119
RESULT 12
US-08-331-397B-46
Sequence 46, Application US/08311397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

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?
?      TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..119
? OTHER INFORMATION:
? OTHER INFORMATION: 56PI'CL Variable Heavy chain (V-H)"
US-08-331-397B-46

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Query Match	78.4%	Score 489	DB 2	Length 119
Best Local Similarity	79.0%	Pred. No.	6,4e-41	
Matches	94	Conservative	18	Indels 0
		Mismatches	0	Gaps 0

[illegible]

RESULT 13
 US-08-759-804A-46
 Sequence 46, Application US/08759804A
 Patent No. 5990296
 GENERAL INFORMATION:
 APPLICANT: Pastan, Ira
 APPLICANT: Willingham, Mark
 APPLICANT: Fitzgerald, David J.
 APPLICANT: Brinkmann, Ulrich
 APPLICANT: Pai, Lee
 TITLE OF INVENTION: Tumor-Specific Antibody Fragments
 TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,804A
 FILING DATE: 03-DEC-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/331,398
 FILING DATE: 28-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,269
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen L.
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 015280-126140US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid

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? STRANDEDNESS:
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..119
? OTHER INFORMATION:
? OTHER INFORMATION: 56PI/CL Variable Heavy chain (V-H)"
US-08-759-804A-46

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Query Match	78.4%	Score 489	DB 2	Length 119
Best Local Similarity	79.0%	Pred. No. 6,4e-41		
Matches 94	Conservative 7	Mismatches 18	Indels 0	Gaps 0

[illegible]

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1      RESULT 14
2      US-09-227-693-46
3      : Sequence 46, Application US/09227693
4      : Patent No. 6287562
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: PASTAN, Ira
8      : APPLICANT: BENHAR, Itai
9      : APPLICANT: PADLAN, Eduardo A.
10     : APPLICANT: JUNG, Sun-Hee
11     : APPLICANT: LEE, Byungkook
12     : TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
13     : TITLE OF INVENTION: FRGMENTS, FUSION PROTEINS, AND USES THEREOF
14     :
15     : NUMBER OF SEQUENCES: 50
16     :
17     : CORRESPONDENCE ADDRESS:
18     : ADDRESSEE: Townsend and Townsend Kourile and Crew
19     : STREET: Stewart Street Tower, One Market Plaza
20     : City: San Francisco
21     : STATE: California
22     : COUNTRY: US
23     : ZIP: 94105-1493
24     :
25     : COMPUTER READABLE FORM:
26     : MEDIUM TYPE: Floppy disk
27     : COMPUTER: IBM PC compatible
28     : OPERATING SYSTEM: PC-DOS/MS-DOS
29     : SOFTWARE: PatentIn Release #1.0, Version #1.25
30     :
31     : CURRENT APPLICATION DATA:
32     : APPLICATION NUMBER: US/09/227,693
33     : FILING DATE:
34     :
35     : PRIOR APPLICATION DATA:
36     : APPLICATION NUMBER: 08/331,396
37     : FILING DATE:
38     :
39     : PRIOR APPLICATION DATA:
40     : APPLICATION NUMBER: US 07/767,331
41     : FILING DATE: 30-SEP-1991
42     : PRIOR APPLICATION DATA:
43     : APPLICATION NUMBER: US 07/596,289
44     : FILING DATE: 12-OCT-1990
45     : ATTORNEY/AGENT INFORMATION:
46     : NAME: Weber, Ellen Lauver
47     : REGISTRATION NUMBER: 32,762
48     : REFERENCE/DOCKET NUMBER: 15280-126-1-3
49     : TELECOMMUNICATION INFORMATION:
50     : TELEPHONE: (415) 543-9600
51     : TELEFAX: (415) 543-5043
52     : INFORMATION FOR SEQ ID NO: 46:
53     : SEQUENCE CHARACTERISTICS:
54     : LENGTH: 119 amino acids
55     : TYPE: amino acid
56     : STRANDEDNESS: single
57     : TOPOLOGY: linear

```

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56P1-CL VH region"
US-09-227-693-46

Query Match 78.4%; Score 489; DB 3; Length 119;
Best Local Similarity 79.0%; Pred. No. 6.4e-41;
Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYMSWVROAPGKGLEWVAIYSSGGSGTYY 60
DB 1 EVOLVESGGGVVPGGSLRVSCAAGFTFSSYAMHWVROAPGKGLEWVAIYSDGSNKYY 60
QY 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRYKLGTYYFPMWGGTLLTVSS 119
DB 61 ADSVKGRFTISRNSKNTLYLQWRSLRAEDTAVYYCTKRGVLYYSGSYHMFDPWGGTLLTVSS 119

RESULT 15

US-08-428-197-1
Sequence 1, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
US-08-428-197-1
Query Match 78.4%; Score 489; DB 2; Length 125;

Best Local Similarity 76.0%; Pred. No. 6.7e-41;
Matches 95; Conservative 12; Mismatches 12; Indels 6; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYMSWVROAPGKGLEWVAIYSSGGSGTYY 60
DB 1 EVOLVESGGGVVPGGSLRVSCAAGFTFSSYAMHWVROAPGKGLEWVAIYSDGSNKYY 60
QY 61 SDSVKGRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRYKLGTYYFPMWGGTLLTVSS 114
DB 61 ADSVKGRFTISRNSKNTLYLQWRSLRAEDTAVYYCTKRGVLYYSGSYHMFDPWGGTLLTVSS 120
QY 115 LTYS 119
DB 121 VTYS 125

RESULT 16

PCT-US93-10555-1
Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
PCT-US93-10555-1
Query Match 78.4%; Score 489; DB 5; Length 125;
Best Local Similarity 76.0%; Pred. No. 6.7e-41;
Matches 95; Conservative 12; Mismatches 12; Indels 6; Gaps 2;

Db 61 ADSVKGRFTISRDNASKNTLYLQNMSLRAEDTAVYYCTKGQVLYYSGSGYHWPDMGQCTL 120
QY 115 LTVSS 119
:||||
Db 121 VTVSS 125

RESULT 17
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: CO. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-20

Query Match 78.1%; Score 487.5; DB 3; Length 135;
Best Local Similarity 82.4%; Pred. No. 1e-40; Indels 3; Gaps 2;
Matches 98; Conservative 6; Mismatches 12;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAYISSGSGGTTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVOLVESGGGLVPGGSLRLSCAASGFTSTYAMSWVRQAPGKLEWVAISITGGS-TYY 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGRFTISRDNASKNTLYLQNMSLRAEDSAVYFCTRVKLGTYYPDSWGQGLTVVSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 PDSVKGRFTISRDNASKNTLYLQNMSLRAEDTAVYYCARDYDQ--YFDYWGQGLTVVSS 135
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 18

PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-4

Query Match 78.1%; Score 487.5; DB 5; Length 443;
Best Local Similarity 82.4%; Pred. No. 3.9e-40; Indels 3; Gaps 2;
Matches 98; Conservative 6; Mismatches 12;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAYISSGSGGTTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFTSTYAMSWVRQAPGKLEWVAISITGGS-TYY 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGRFTISRDNASKNTLYLQNMSLRAEDSAVYFCTRVKLGTYYPDSWGQGLTVVSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 PDSVKGRFTISRDNASKNTLYLQNMSLRAEDTAVYYCARDYDQ--YFDYWGQGLTVVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 19
US-07-934-373C-21
; Sequence 21, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAYISSGSGGTTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVOLVESGGGLVPGGSLRLSCAASGFTSTYAMSWVRQAPGKLEWVAISITGGS-TYY 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGRFTISRDNASKNTLYLQNMSLRAEDSAVYFCTRVKLGTYYPDSWGQGLTVVSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 PDSVKGRFTISRDNASKNTLYLQNMSLRAEDTAVYYCARDYDQ--YFDYWGQGLTVVSS 135
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-21

Query Match 77.8%; Score 485.5; DB 2; Length 122;
Best Local Similarity 77.0%; Pred. No. 1,4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVLVESGDDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWVAYISSGSGGTTY 60
DB 1 EVLVESGGGLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAYISSGSGGTTY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYKLG---TYPDSMGQGLTVTV 117
DB 61 ADSVKRFTISRDNKNTLYLQWRSLRAEDTAVYCARGRVGYSLGLDYWGQGLTVTV 120

QY 118 SS 119
DB 121 SS 122

RESULT 20
US-08-437-642B-21
Sequence 21, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-21

Query Match 77.8%; Score 485.5; DB 3; Length 122;
Best Local Similarity 77.0%; Pred. No. 1,4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVLVESGDDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWVAYISSGSGGTTY 60
DB 1 EVLVESGGGLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAYISSGSGGTTY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYKLG---TYPDSMGQGLTVTV 117
DB 61 ADSVKRFTISRDNKNTLYLQWRSLRAEDTAVYCARGRVGYSLGLDYWGQGLTVTV 120
QY 118 SS 119
DB 121 SS 122

RESULT 21
US-08-146-206C-21
Sequence 21, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-21

Query Match 77.8%; Score 485.5; DB 4; Length 122;
Best Local Similarity 77.0%; Pred. No. 1.4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAAGFTFSSYAMSWVRQAPGKLEWVSISGGSGTTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--TYFPDSMGQGLTVY 117
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYTCARGRVGYSLSGLYDYGQGLTVY 120

QY 118 SS 119
DB 121 SS 122

RESULT 22
US-09-705-686-21
Sequence 21, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-705-686-21

Query Match 77.8%; Score 485.5; DB 4; Length 122;
Best Local Similarity 77.0%; Pred. No. 1.4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAAGFTFSSYAMSWVRQAPGKLEWVSISGGSGTTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--TYFPDSMGQGLTVY 117
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYTCARGRVGYSLSGLYDYGQGLTVY 120

QY 118 SS 119
DB 121 SS 122

RESULT 23
US-09-705-392A-21
Sequence 21, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-No. 6719971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-705-392A-21

Query Match 77.8%; Score 485.5; DB 4; Length 122;
Best Local Similarity 77.0%; Pred. No. 1.4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAAGFTFSSYAMSWVRQAPGKLEWVSISGGSGTTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--TYFPDSMGQGLTVY 117
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYTCARGRVGYSLSGLYDYGQGLTVY 120

Db 61 ADVKGRFTSRNSKNTLYLQNSLRADTAAYYCARGRVGLSLGLYDMGQGLTVTV 120
QY 118 SS 119
Db 121 SS 122

RESULT 24
PCT-US93-07832-21
Sequence 21, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 70922PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-21

Query Match 77.8%; Score 485.5; DB 5; Length 122;
Best Local Similarity 77.0%; Pred. No. 1.4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;
QY 1 EVOLVSGDFFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAIYSSGGSGTYY 60
Db 1 EVOLVSSGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGGSGTYY 60
QY 61 SDVSKGRFTSRNSKNTLYLQNSLRADTAAYYCARGRVGLSLGLYDMGQGLTVTV 117
Db 61 ADVKGRFTSRNSKNTLYLQNSLRADTAAYYCARGRVGLSLGLYDMGQGLTVTV 120
QY 118 SS 119
Db 121 SS 122

RESULT 25
US-09-069-821-3

Sequence 3, Application US/09069821
Patent No. 632332
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
APPLICANT: MANG, MAOLIANG
APPLICANT: SHORR, ROBERT
APPLICANT: WHITLOW, MARC
APPLICANT: LEE, LHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,821
FILING DATE: 30-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-069-821-3

Query Match 77.8%; Score 485.5; DB 3; Length 263;
Best Local Similarity 73.8%; Pred. No. 3.4e-40;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;
QY 1 EVOLVSGDFFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAIYSSGGSGT 58
Db 130 EVOLVSSGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGGSGT 189
QY 59 YVSDVSKGRFTSRNSKNTLYLQNSLRADTAAYYCARGRVGLSLGLYDMGQGLTVTV 109
Db 190 YVSDVSKGRFTSRNSKNTLYLQNSLRADTAAYYCARGRVGLSLGLYDMGQGLTVTV 249
QY 110 GQGLTVTVSS 119
Db 250 GQGLTVTVSS 259

RESULT 26

US-09-956-086-3
; Sequence 3, Application US/09956086
; Patent No. 6743896
; GENERAL INFORMATION:
; APPLICANT: FILIPULA, DAVID
; MANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,086
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,821
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977.2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-086-3
Query Match 77.8%; Score 485.5; DB 4; Length 263;
Best Local Similarity 73.8%; Pred. No. 3.4e-40;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;
QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFHYMSWVRQAPGKLEWNAVYS--SGSGST 58
Db 130 EVOLVESGGGLVPGGSLRVSCAAGFTFSSYMSWVRQAPGKLEWNAVYSISGKTDCGST 189
QY 59 YSDSVAGRFTISRDNSKNTLYIQMRSLEAEDSAVYFCRRVKLGT-----YFPDSW 109
Db 190 YVADSVAGRFTISRDNSKNTLYIQMNSLEAEDTAVYYCAARGXKSLSGXYHHYFDYW 249
QY 110 GGGTLTVSS 119
Db 250 GGGTLTVSS 259

RESULT 27
US-09-956-087-3

; Sequence 3, Application US/09956087
; Patent No. 6743908
; GENERAL INFORMATION:
; APPLICANT: FILIPULA, DAVID
; MANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,087
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,821
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977.2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: not relevant
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-087-3
Query Match 77.8%; Score 485.5; DB 4; Length 263;
Best Local Similarity 73.8%; Pred. No. 3.4e-40;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;
QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFHYMSWVRQAPGKLEWNAVYS--SGSGST 58
Db 130 EVOLVESGGGLVPGGSLRVSCAAGFTFSSYMSWVRQAPGKLEWNAVYSISGKTDCGST 189
QY 59 YSDSVAGRFTISRDNSKNTLYIQMRSLEAEDSAVYFCRRVKLGT-----YFPDSW 109
Db 190 YVADSVAGRFTISRDNSKNTLYIQMNSLEAEDTAVYYCAARGXKSLSGXYHHYFDYW 249
QY 110 GGGTLTVSS 119
Db 250 GGGTLTVSS 259

RESULT 28
US-09-420-592A-6
; Sequence 6, Application US/09420592A

Db 190 YVADSVKGRFTISRDNKNTLYLQNMNSLRADTAAYVYCAKGRGXSLSGYHHYHFDYW 249
QY 110 GGGTLTVSS 119
Db 250 GGGTLTVSS 259

RESULT 31

US-09-840-459-82
; Sequence 82, Application US/09840459
; Patent No. 6695550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855,1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-82

Query Match 77.7%; Score 485; DB 4; Length 123;

Best Local Similarity 76.4%; Pred. NO. 1.6e-40; Indels 4; Gaps 1;
Matches 94; Conservative 9; Mismatches 16;

QY 1 EVOLVESGDFVQPGSLRVSCAAGFAFSHYAMSWVROAPGKLEWVAYISSGSGTTY 60
Db 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVROAPGKLEWVSAISSGTYTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQNMNSLRADTAAYVYCAKGRGXSLSGYHHYHFDYW 116
Db 61 ADSVKGRFTISRDNKNTLYLQNMNSLRADTAAYVYCAKGRGXSLSGYHHYHFDYW 120
QY 117 VSS 119
Db 121 VSS 123

RESULT 32

US-09-497-625A-82
; Sequence 82, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855,1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-82

Query Match 77.7%; Score 485; DB 4; Length 123;

Best Local Similarity 76.4%; Pred. NO. 1.6e-40; Indels 4; Gaps 1;
Matches 94; Conservative 9; Mismatches 16;

QY 1 EVOLVESGDFVQPGSLRVSCAAGFAFSHYAMSWVROAPGKLEWVAYISSGSGTTY 60
Db 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVROAPGKLEWVSAISSGTYTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQNMNSLRADTAAYVYCAKGRGXSLSGYHHYHFDYW 116
Db 61 ADSVKGRFTISRDNKNTLYLQNMNSLRADTAAYVYCAKGRGXSLSGYHHYHFDYW 120
QY 117 VSS 119
Db 121 VSS 123

RESULT 33

US-08-983-607-32
; Sequence 32, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESS: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

? MOLECULE TYPE:
? DESCRIPTION: polypeptide
?
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens (melanoma patient immu-
? ORGANISM: nized with autologous tumor cells)
? INDIVIDUAL ISOLATE: peripheral blood lymphocytes
? IMMEDIATE SOURCE:
? LIBRARY: DM414 gcfv antibodies obtained from
? LIBRARY: fuses fusion phage construct
? CLONE: V86
?
? FEATURE:
? NAME:KEY: heavy chain and linker
?
? US-08-983-607-32

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Query Match	77.5%	Score	483.5	DB	3	length	140
Best Local Similarity	75.0%	Pred	No	2.7e-40			
Matches	93	Conservative	10	Mismatches	16	Indels	5
						Gaps	1

[illegible]

```

US-08-974-899-6
US-RESULT 34
; Sequence 6, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-COL1a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-6

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Query Match	77.1%	Score 481;	DB 3;	Length 113;
Best Local Similarity	79.0%	Prod. No. 3.7e-40;		
Matches	94;	Conservative	6;	Mismatches 13; Indels 6; Gaps 1.

Qy	1	EVOLVESGCDLVQFGSLRVSCAASGFAFSAHYSAMWVQAQFGKGLNAVYISGSGGGTY	60
Db	1	EVOLVESGGGLVQFGSLRLSCAASGFFSSYAMSWVQAQFGKGLNAVYISGGDGSTTY	60
Qy	61	SDSVYGRFTTIRDSKNTLYLQMRSLRAEDSAVYECTVUKLTGYFDSWGQSTLLTVSS	119
Db	61	ADSVYGRFTTIRDSKNTLYLQMRSLRAEDRAVYICAR-----GFDVWGQSTLLTVSS	113

RESULT 35 798-6
US-09-795-798-6
Sequence 6, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD14 Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpactin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-795-798-6

```

Query Match          77.1% Score 481; DB 4; Length 113;
Best Local Similarity 79.0%; Pred. No. 3,7e-40;
Matches 94; Conservative 6; Mismatches 13; Indels 6; Gaps 1.

QY 1 EVLVESGSGDPEVDPGSGSLRVSCAASGAFASHYAMSWROABGKGLEWAVYISGGSGTTY 60
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 EVLVESGGGGLVQVGSGSLRSCAASGTFPFSYAMSWROABGKGLEWAVISGGSGTTY 60
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 61 SDSYKGRFTISRDNASKTLYIQMSLRAEDSAVYFCTRVLKGTTFPDSWGCGTLLTVSS 119
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 61 ADSYKGRFTISRDNASKTLYIQMSLRAEDYAVYCAR-----GFDYWGCGTLLTVSS 113
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 36
US-09-025-769B-38
; Sequence 38, Application US/09025769B
; Patent No. 6300064

```

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-38

Query Match 77.0%; Score 480.5; DB 3; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVOLVESGGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAISSGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVAISSGGSGTTY 60

QY 61 SDSVKGRTISRNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYFPDSWGQGTLLTVSS 119
DB 61 ADSVKGRTISRNSKNTLYLQMRSLRAEDTAVYYCARWGDDGYANDYGGQGTLLTVSS 120

RESULT 37
US-09-025-769B-63
Sequence 63, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-63

Query Match 77.0%; Score 480.5; DB 3; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVOLVESGGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAISSGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVAISSGGSGTTY 60

QY 61 SDSVKGRTISRNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYFPDSWGQGTLLTVSS 119
DB 61 ADSVKGRTISRNSKNTLYLQMRSLRAEDTAVYYCARWGDDGYANDYGGQGTLLTVSS 120

RESULT 38
US-09-490-070A-38
Sequence 38, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAniff
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-490-070A-38

Query Match 77.0%; Score 480.5; DB 4; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVOLVSSGGDFVOPGSLRVSCAAGFAFSHYAMSVWRQAPGKLEWVAYISGSGSTYY 60
Db 1 EVOLVSSGGDLVOPGSLRVSCAAGFTSYAMSVWRQAPGKLEWVSAISGSGSTYY 60
61 SDVKGRTISRDNKNTLYLQWRSRAEDSAVYFCTR-VKLGTYFDSMGOSTLLTVSS 119
61 ADSVKGRTISRDNKNTLYLQWRSRAEDTAIVYCARWGDSGFYAMDYWGCGTLTVSS 120

RESULT 39
US-09-490-070A-63
Sequence 63, Application US/09490070A
Patent No. 656248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Laming
Motoney, Simon
Pleckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-09-490-070A-63

Query Match 77.0%; Score 480.5; DB 4; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVOLVSSGGDFVOPGSLRVSCAAGFAFSHYAMSVWRQAPGKLEWVAYISGSGSTYY 60
Db 1 EVOLVSSGGDLVOPGSLRVSCAAGFTSYAMSVWRQAPGKLEWVSAISGSGSTYY 60
61 SDVKGRTISRDNKNTLYLQWRSRAEDSAVYFCTR-VKLGTYFDSMGOSTLLTVSS 119
61 ADSVKGRTISRDNKNTLYLQWRSRAEDTAIVYCARWGDSGFYAMDYWGCGTLTVSS 120

RESULT 40
US-09-490-153-38
Sequence 38, Application US/09490153
Patent No. 670646
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Laming
Motoney, Simon
Pleckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-490-153-38

Query Match 77.0%; Score 480.5; DB 4; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:20:33 ; Search time 229.978 Seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-9

Perfect score: 624
Sequence: 1 EVQLVESGGDFVQPGSSLRV.....KLGTYYFDSWGCGTLLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	579	92.8	130 14	US-10-265-713-18 Sequence 18, Appl
3	579	92.8	130 14	US-10-166-626-18 Sequence 18, Appl
4	569	91.2	130 9	US-09-764-304-8 Sequence 8, Appl
5	569	91.2	130 14	US-10-265-713-8 Sequence 8, Appl
6	569	91.2	130 14	US-10-166-626-8 Sequence 8, Appl
7	499	80.0	119 14	US-10-044-896-6 Sequence 6, Appl
8	498	79.8	119 9	US-09-811-123-3 Sequence 3, Appl
9	498	79.8	119 14	US-10-268-501-6 Sequence 6, Appl
10	498	79.8	119 15	US-10-608-626-6 Sequence 6, Appl
11	498	79.8	119 15	US-10-600-152-15 Sequence 15, Appl
12	498	79.8	119 16	US-10-619-754-6 Sequence 6, Appl
13	495.5	79.4	120 17	US-10-835-641-4 Sequence 4, Appl

14	493.5	79.1	224 16	US-10-128-520-148 Sequence 148, App
15	492	78.8	313 15	US-10-291-265-427 Sequence 427, App
16	489	78.4	143 15	US-10-469-304-17 Sequence 17, Appl
17	488.5	78.3	220 16	US-10-128-520-156 Sequence 156, App
18	487.5	78.1	443 9	US-09-917-410-4 Sequence 4, Appl
19	487	78.0	121 15	US-10-275-046-78 Sequence 78, Appl
20	487	78.0	123 14	US-10-269-805-59 Sequence 59, Appl
21	487	78.0	123 10	US-09-880-748-1953 Sequence 1953, App
22	487	78.0	247 10	US-10-293-418-1953 Sequence 184, App
23	486.5	78.0	136 11	US-09-837-306-184 Sequence 184, App
24	486.5	78.0	136 14	US-10-045-674-487 Sequence 487, App
25	486.5	78.0	367 14	US-10-045-674-453 Sequence 453, App
26	486.5	78.0	368 11	US-09-837-306-196 Sequence 196, App
27	485.5	77.8	122 19	US-10-835-641-21 Sequence 21, Appl
28	485.5	77.8	263 9	US-09-956-086-3 Sequence 3, Appl
29	485.5	77.8	263 9	US-09-956-087-3 Sequence 3, Appl
30	485.5	77.8	283 9	US-09-983-580-6 Sequence 6, Appl
31	485.5	77.8	283 9	US-09-983-580-6 Sequence 6, Appl
32	485	77.7	123 9	US-09-840-459-82 Sequence 82, Appl
33	485	77.7	123 16	US-10-766-773-82 Sequence 82, Appl
34	485	77.7	123 16	US-10-766-610-82 Sequence 82, Appl
35	485	77.7	123 16	US-10-733-563-82 Sequence 82, Appl
36	485	77.7	248 10	US-09-880-748-1421 Sequence 1421, App
37	485	77.7	248 14	US-10-293-418-1421 Sequence 1421, App
38	485	77.7	251 17	US-10-800-197-15 Sequence 15, Appl
39	484.5	77.6	118 15	US-10-474-832-68 Sequence 68, Appl
40	484.5	77.6	118 15	US-10-474-832-69 Sequence 69, Appl
41	484.5	77.6	122 15	US-10-251-085B-93 Sequence 93, Appl
42	484.5	77.6	122 16	US-10-737-252-93 Sequence 93, Appl
43	484.5	77.6	124 14	US-10-040-244-16 Sequence 16, Appl
44	484.5	77.6	177 16	US-10-693-629-64 Sequence 64, Appl
45	484.5	77.6	447 15	US-10-474-832-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAI, HIROMASA
; APPLICANT: KIMURA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER APPLICATION NUMBER: 2001-01-19
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
; US-09-764-304-18

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Query Match          92.8%; Score 579; DB 9; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-44;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      1 EVOLVSSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQAPGKLEWVAIYSSGSGSTYY 60
      11 EVTLVSSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQTPARLEWVAIYSSGSGSTYY 70
      61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 119
      71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 129

Db

RESULT 2
US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
; US-10-265-713-18

Query Match          92.8%; Score 579; DB 14; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-44;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      1 EVOLVSSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQAPGKLEWVAIYSSGSGSTYY 60
      11 EVTLVSSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQTPARLEWVAIYSSGSGSTYY 70
      61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 119
      71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 129

Db

RESULT 3
US-10-166-626-18
; Sequence 18, Application US/10166626
; Publication No. US2003016876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; US-10-166-626-18
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; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
; US-10-166-626-18

Query Match          92.8%; Score 579; DB 14; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-44;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      1 EVOLVSSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQAPGKLEWVAIYSSGSGSTYY 60
      11 EVTLVSSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQTPARLEWVAIYSSGSGSTYY 70
      61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 119
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RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
; US-09-764-304-8
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Query March	91.2%	Score 569;	DB 9;	Length 130;
Best Local Similarity	90.8%;	Pred. No. 8.2e-44;		
Matches 108; Conservative	5;	Mismatches 6;	Indels 0;	Gaps 0;

Qy	Db
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71	12
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RESULT 5
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; Sequence 8, Application US/10265713
; Publication No. US20030095964A1
; Comment: INFORMATION

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APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAI, HIROMASA
APPLICANT: KOMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265, 713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225, 322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454, 680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408, 133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292, 178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947, 674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-8

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Query Match	91.2%	Score 569	DB 14	Length 130
Best Local Similarity	90.8%	Pred. No. 8.2e-44		
Matches 108	Conservative 5	Mismatches 6	Indels 0	Gaps 0

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 11 EVLVTEGCGFVYVPGGSLIRVSCAASGAFPHYMSWVROAPGGLGVLEVMVYISSGGSGGTTY 70
 Db 11 EVLVTEGCGFVYVPGGSLIRVSCAASGAFPHYMSWVROAPGGLGVLEVMVYISSGGSGGTTY 70
 QY 61 SDSVKGRFTISRDNSKNTLLYLQMRSLRAEDSNAVYFCTRYVLGTYTYSDSGGQGLTLTVSS 119
 71 SDSVKGRFTISRDNSKNTLLYLQMRSLRAEDSNAVYFCTRYVLGTYTYSDSGGQGLTLTVSS 129

US-10-166-626-8
 RESULT 6
 ; Sequence 8, Application US/10166622
 ; Publication No. US20030156876A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHITTAR, KENYA
 ; APPLICANT: HANAI, NOBUO
 ; APPLICANT: HASEGAWA, MAMORU
 ; APPLICANT: MIYAJI, HIROMASA
 ; APPLICANT: KOMANA, YOSHIOHISA

```

1  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBOD
2  FILE REFERENCE: 249-101
3  CURRENT APPLICATION NUMBER: US/10/166,626
4  CURRENT FILING DATE: 2002-06-12
5  PRIOR APPLICATION NUMBER: US/09/225,322B
6  PRIOR FILING DATE: 1999-01-05
7  PRIOR APPLICATION NUMBER: US 08/454,680
8  PRIOR FILING DATE: 1995-05-31
9  PRIOR APPLICATION NUMBER: US 08/408,133
10 PRIOR FILING DATE: 1995-03-21
11 PRIOR APPLICATION NUMBER: US 08/292,178
12 PRIOR FILING DATE: 1994-08-17
13 PRIOR APPLICATION NUMBER: US07/947,674
14 PRIOR FILING DATE: 1992-09-17
15 PRIOR APPLICATION NUMBER: JP 3-238375
16 PRIOR FILING DATE: 1991-09-18
17 NUMBER OF SEQ ID NOS: 19
18 SOFTWARE: PatentIn Ver. 2.0
19 SEQ ID NO 8
20 LENGTH: 130
21 TYPE: PRT
22 ORGANISM: Artificial Sequence
23 FEATURE:
24 OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
25 US-10-166-626-8

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Query Match Similarity	91.2%	Score 569;	DB 14;	Length 130;
Best Local Similarity	90.8%	Pred. No. 8.2e-44;		
Matches 108; Conservative	5;	Mismatches 6;	Indels 0;	Gaps 0

QY 1 EVLVESGGDPPVPGGSLGVSCAAGFASHSHAMSVVRQAPKGGEMVYIISGGSGITY 60
11 EYLVESGGDPPVPGGSLGVSCAAGFASHSHAMSVVRQAPKGGEMVYIISGGSGITY 70
Db
QY 61 SDSVKRPFITSRDSSKNITLYLQMRSLRAADSAVFECKYKLGITYYFDSGGGTLTVSS 119
71 SDSVKRPFITSRNANNTLYLQMRSLRSDSAAMFECKYKLGITYYFDSGGGTLTVSS 129

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RESULT 7
US-10-044-896-6
; Sequence 6, Application US/10044896
; Publication No. US20030166228A1
; GENERAL INFORMATION:
; APPLICANT: Chunchazapal, Anan
; APPLICANT: Kim, jin K.
; APPLICANT: Stewart, Timothy
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
; FILE REFERENCE: GENEENT. 074A
; CURRENT APPLICATION NUMBER: US/10/044.896
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: 60/227075
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FaelsIQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-044-896-6

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Query Match	80.0%	Score 499,	DB 14:	Length 119,
Best Local Similarity	80.7%	Pred. No. 1.6e-37;		
Matches 96;	Conservative	8;	Mismatches 13;	Indels 2;
				Gaps 1.

QY 1 EVQLVDSGGDLPFOGGSLFLVSCAASGAPASHYAMSVRA PKSGLEEMVAIYSSGGSGTY 60
Db 1 EVQLVDSGGGLVOPGGSLFLVSCAASGFTTSSAYAMSVRAOPKSGLEEMVAIYSGDGGSTTY 60
QY 61 SDSVKGRFTISRDNSKNTLYIOMRSIRPEDSAVYFCTRYKLGTYFPDSMGQGITLTVSS 119
Db 61 ASDVKGKRFITSDNSKNTLYIOMNSIRPADITVYVCARQVQ--YDWDGQGITLTVSS 117

RESULT 8
US-09-811-123-3
Sequence 3, Application US/09811123
Patent No. US20020001587A1
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Slikowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERB2
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONUGATES
FILE REFERENCE: GENENT.073A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-3

Query Match 79.8%; Score 498; DB 9; Length 119;
Best Local Similarity 79.8%; Pred. No. 1,9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVOPGGSILRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
Db 1 EVOLVSGGGLVOPGGSILRVSCAAGFTFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLGTYFPDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGRVGLYDVMGQGLTLTVSS 119

RESULT 9
US-10-268-501-6
Sequence 6, Application US/10268501
Publication No. US20030086924A1
GENERAL INFORMATION:
APPLICANT: Slikowski, Mark X.
TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1467R2P1
CURRENT APPLICATION NUMBER: US/10/268,501
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 09/602,812
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 6
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: heavy chain consensus sequence
US-10-268-501-6

Query Match 79.8%; Score 498; DB 14; Length 119;
Best Local Similarity 79.8%; Pred. No. 1,9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVOPGGSILRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
Db 1 EVOLVSGGGLVOPGGSILRVSCAAGFTFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLGTYFPDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGRVGLYDVMGQGLTLTVSS 119

RESULT 10
US-10-608-626-6
Sequence 6, Application US/10608626
Publication No. US20040013667A1
GENERAL INFORMATION:
APPLICANT: Kelsey, Stephen M.
APPLICANT: Slikowski, Mark X.
TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1467R2P2
CURRENT APPLICATION NUMBER: US/10/608,626
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 10/268,501
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 09/602,812
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 6
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: heavy chain consensus sequence
US-10-608-626-6

Query Match 79.8%; Score 498; DB 15; Length 119;
Best Local Similarity 79.8%; Pred. No. 1,9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVOPGGSILRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
Db 1 EVOLVSGGGLVOPGGSILRVSCAAGFTFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLGTYFPDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGRVGLYDVMGQGLTLTVSS 119

RESULT 11
US-10-600-152-15
Sequence 15, Application US/10600152
Publication No. US20040037824A1
GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US/10/600,152
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: 09/648,067
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: VH consensus sequence
US-10-600-152-15

Query Match 79.8%; Score 498; DB 15; Length 119;
Best Local Similarity 79.8%; Pred. No. 1,9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

[illegible]

RESULT 12
US-10-619

```

? Sequence 6 Application US/10619754
? Publication NO. US20040106161A1
? GENERAL INFORMATION:
? APPLICANT: Genentech, Inc.
? APPLICANT: Koll, Hans
? APPLICANT: Boesenmaier, Birgit
? APPLICANT: Muller, Hans-Jochim
? APPLICANT: Slikowski, Mark
? APPLICANT: Kelsey, Stephen
? TITLE OF INVENTION: Methods For Identifying Tumors That Are
? TITLE OF INVENTION: Responsive To Treatment With Anti-ErbB2 Antibodies
? FILE REFERENCE: 39766-0114A
? CURRENT APPLICATION NUMBER: US/10/619,754
? CURRENT FILING DATE: 2003-07-14
? PRIOR APPLICATION NUMBER: US 60/396,290
? PRIOR FILING DATE: 2002-07-15
? PRIOR APPLICATION NUMBER: US 60/480,043
? PRIOR FILING DATE: 2003-06-20
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 6
? LENGTH: 119
? TYPE: PRT
? ORGANISM: Homosapiens
? OS-10-619-754-6

```

Query Match	79.8%	Score	498	DB	16	Length	119
Similarity	79.8%	Pred. NO.	1.9e-37				
Best Local							
Matches	95	Conservative	8	Mismatches	16	Indels	0
						Gaps	0

[illegible]

RESULT 13
US-10-835

Sequence 4, Application US/10835611
Publication No. US20040236078A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/835,641
FILING DATE: 30-Apr-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

```

1      APPLICATION NUMBER: US/09/705,398
2      FILING DATE: 02-NOV-2000
3      APPLICATION NUMBER: 08/146206
4      FILING DATE: 17-NOV-1993
5      APPLICATION NUMBER: 07/715272
6      FILING DATE: 14-JUN-1991
7      ATTORNEY/AGENT INFORMATION:
8
9      NAME: Lee, Wendy M.
10     REGISTRATION NUMBER: 40,378
11     REFERENCE/DOCKET NUMBER: P07039PID2
12
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: 650/225-1994
15     TELEFAX: 650/952-9881
16
17     INFORMATION FOR SEQ ID NO: 4:
18
19     SEQUENCE CHARACTERISTICS:
20
21     LENGTH: 120 amino acids
22     TYPE: Amino Acid
23     TOPOLOGY: Linear
24
25     SEQUENCE DESCRIPTION: SEQ ID NO: 4:
26     US-10-835-641-4

```

Query Match	79.4%	Score 495.5	DB 17	Length 120
Best Local Similarity	80.8%	Pred. No. 3.3e-37		
Matches 97, Conservative	7	Mismatches 15	Indels 1	Gaps 1

QY 1 EVQLVESGGSDPFPQGGSLRVSCAAAGCFAPFASHAMWVRCAPEKGLMEVAVIISGGSGITY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAAGSFTFSDYAVMWVRQAPKGLMEVAVISNGSDITY 60

QY 61 SDYKGRFTISRDNSKNTLYLQMRLRDEPDAVSCTRHKLTGY -FDSMGQSTLLTVSS 119

Db 61 ADSVKGRTTISDSDSKNTLYLQMNSLRPEDTAVITCAIRGRGAVSYFDWMGGSTLVSS 120

RESULT 14
US-10-128

```

; Sequence 148, Application US/10128520
; Publication No. US200400105862A1
;
; GENERAL INFORMATION:
;
; APPLICANT: PAN et al.
;
; TITLE OF INVENTION: Human TIMP-1 Antibodies
;
; FILE REFERENCE: 02973.00073
;
; CURRENT APPLICATION NUMBER: US/10/128,520
;
; CURRENT FILING DATE: 2002-04-24
;
; PRIOR APPLICATION NUMBER: US 60/285,683
;
; PRIOR FILING DATE: 2001-04-24
;
; NUMBER OF SEQ ID NOS: 381
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 148
;
; LENGTH: 224
;
; TYPE: prt
;
; ORGANISM: Homo sapiens
;
; US-10-128-520-148

```

Query Match	79.1%	Score 493.5	DB 16	Length 224
Best Local Similarity	79.5%	Pred. NO. 9.4e-37		
Matches 97	Conservative 7	Mismatches 13	Indels 5	Gaps 2

QY	1	EVQLVDSGGDFFQPGSGSLRVSCAAGSPAFESHYAMSVVRCA	PGKGLGEMVAVISGSGSGTYY	60
Db	1	QVQLVDSGGGLVQPGSGSLRSCAAGSFTHSYAMSVVRCA	PGKGLGEMVAVISGSGSGTYY	60
QY	61	SDSVKGRFTISPDNKNKNTLYLQMRSLRAEDSAVYECTRAKGLTYY	---PDSMCOGTLTV	117
Db	61	ADSVKGRFTISPDNKNKNTLYLQMRSLRAEDDAVYCAR	--LDTYYPDLFDIMCOGTLTV	118

QY	118	SS	119
Db	119	SS	120

```
RESULT 15
US-10-291-265-427
; Sequence 427, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-427

Query Match      78.8%; Score 492; DB 14; Length 313;
Best Local Similarity 74.8%; Pred. No. 1.8e-36;
Matches 95; Conservative 9; Mismatches 15; Indels 8; Gaps 1;

QY      1 EVOLVESGGDFVQPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKGLVAVYISSGGSGTTY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 EVOLVESGGGLVQPGGSLRVSCAAGFTFSYAMSWVRQAPGKGLVAVSISGGSGTTY 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVFCTRVKLG-----TYTFDSWGQG 112
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYYCAKSHPGYYDSGGSYFDYWGQG 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      113 TLTVVSS 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      181 TLTVVSS 187

RESULT 16
US-10-469-304-17
; Sequence 17, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-304-17

Query Match      78.4%; Score 489; DB 15; Length 143;
Best Local Similarity 78.0%; Pred. No. 1.5e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 4; Gaps 2;
```

```
QY      61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVFCTRVK-LGTY---FDSWGQTLT 116
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      80 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYYCARDHSGSGSYYPYFEDYWGQTLVT 139
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      117 VSS 119
      :|||
Db      140 VSS 142

RESULT 17
US-10-128-520-156
; Sequence 156, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-156

Query Match      78.3%; Score 488.5; DB 16; Length 220;
Best Local Similarity 79.8%; Pred. No. 2.6e-36;
Matches 95; Conservative 9; Mismatches 12; Indels 3; Gaps 2;

QY      1 EVOLVESGGDFVQPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKGLVAVYISSGGSGTTY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 QVOLVESGGGLVQPGGSLRVSCAAGFTFSYAMSWVRQAPGKGLVAVSISGGSGTTY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVFCTRVKLGTYTFDSWGQTLTVSS 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYYCARL-IG--YFDLWGQTLTVVSS 116
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 18
US-09-917-410-4
; Sequence 4, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO, Man S.
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII, Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,410
; FILING DATE: 26-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
```

FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-917-410-4

Query Match 78.1%; Score 487.5; DB 9; Length 443;
Best Local Similarity 82.4%; Pred. No. 6,5e-36;
Matches 98; Conservative 6; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVESGDDPVQPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGTYY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISITGGS-YY 59
QY 61 SDSVKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLTYYFDSDWGQGLTLTVSS 119
DB 60 PSDVKRFTISRDNKNTLYLQWNSLRABEDTAVYACARDYDQ--YFDYWGQGLTLTVSS 116

RESULT 19
US-10-275-046-78
Sequence 78, Application US/10275046
Publication No. US20040019187A1
GENERAL INFORMATION:
APPLICANT: Nagy et al.
TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
FILE REFERENCE: GPCG-P01-260
CURRENT APPLICATION NUMBER: US/10/275,046
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: 00110063.5
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.2
SEQ ID NO 78
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MS-GPC14 VH
US-10-275-046-78

Query Match 78.0%; Score 487; DB 15; Length 121;
Best Local Similarity 78.5%; Pred. No. 1.9e-36;
Matches 95; Conservative 7; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVOLVESGDDPVQPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGTYY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGSGTYY 60
QY 61 SDSVKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLTYY--YFDSDWGQGLTLTVS 118
DB 61 ADSVKRFTISRNSKNTLYLQWNSLRABEDTAVYACARSSMPYGGGFDLMGGGLTVTVS 120
QY 119 S 119
DB 121 S 121

RESULT 20

US-10-269-805-59
Sequence 59, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLIVER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-805-59

Query Match 78.0%; Score 487; DB 14; Length 123;
Best Local Similarity 76.4%; Pred. No. 2e-36;
Matches 94; Conservative 10; Mismatches 15; Indels 4; Gaps 2;

QY 1 EVOLVESGDDPVQPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGTYY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGTYY 60
QY 61 SDSVKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLTYYFDSDWGQGLTLTVS 116
DB 61 ADSVKRFTISRDNKNTLYLQWNSLRABEDTAVYACAKETISFTSGYFDYWGQGLTVT 120
QY 117 VSS 119
DB 121 VSS 123

RESULT 21
US-09-880-748-1953
Sequence 1953, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1953
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1953

Query Match 78.0%; Score 487; DB 10; Length 247;
Best Local Similarity 76.5%; Pred. No. 4e-36;
Matches 91; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDDPVQPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGTYY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGTYY 60
QY 61 SDSVKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLTYYFDSDWGQGLTLTVS 119

APPLICANT: HOET, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 453
LENGTH: 367
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: MALIA3 protein
US-10-045-674-453

Query Match 78.0%; Score 486.5; DB 14; Length 367;
Best Local Similarity 78.3%; Pred. No. 6,6e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

1 EVOLVESGDDPVOGSLRVSCAAGFAPSHYAMSWVROAPGKLEWVAIVSSGSGSTYY 60
23 EVOLVESGGGLVOPGSLRLSCAASGFTFSYAMSWVROAPGKLEWVAIVSSGSGSTYY 82
61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--YYFDSWGCGTLTVSS 119
83 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCAKDEGVAFDIWGCGTMTVSS 142

RESULT 26
US-09-837-306-196
Sequence 196, Application US/09837306
Publication No. US20040029113A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
FILE REFERENCE: DYAX/002
CURRENT APPLICATION NUMBER: US/09/837,306
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 196
LENGTH: 368
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: MALIA3
US-09-837-306-196

Query Match 78.0%; Score 486.5; DB 11; Length 368;
Best Local Similarity 78.3%; Pred. No. 6,6e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

1 EVOLVESGDDPVOGSLRVSCAAGFAPSHYAMSWVROAPGKLEWVAIVSSGSGSTYY 60
23 EVOLVESGGGLVOPGSLRLSCAASGFTFSYAMSWVROAPGKLEWVAIVSSGSGSTYY 82

61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--YYFDSWGCGTLTVSS 119
83 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCAKDEGVAFDIWGCGTMTVSS 142

RESULT 27
US-10-835-641-21
Sequence 21, Application US/10835641
Publication No. US20040236078A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/835,641
FILING DATE: 30-Apr-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-Nov-2000
APPLICATION NUMBER: 08/146206
FILING DATE: 17-Nov-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-Jun-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9681
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-835-641-21

Query Match 77.8%; Score 485.5; DB 17; Length 122;
Best Local Similarity 77.0%; Pred. No. 2,7e-36;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

1 EVOLVESGDDPVOGSLRVSCAAGFAPSHYAMSWVROAPGKLEWVAIVSSGSGSTYY 60
1 EVOLVESGGGLVOPGSLRLSCAASGFTFSYAMSWVROAPGKLEWVAIVSSGSGSTYY 60
61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--YYFDSWGCGTLTV 117
61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCARGVGYSLSGLVDYWGCGTLTV 120

118 SS 119
121 SS 122

RESULT 28
US-09-956-086-3
Sequence 3, Application US/09956086
Patent No. US20020155498A1

GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
MANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. US20020155498A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-086-3
Query Match 77.8%; Score 485.5; DB 9; Length 263;
Best Local Similarity 73.8%; Pred. No. 5.8e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;
QY 1 EVQLVDSGGDFVQPGGSLRLVSCAASGFAFSHYAMSVWRQAPGKGLEWVAIIS--SGSGST 58
DB 130 EVQLVDSGGGLVQPGGSLRLSLCAASGFTFSYAMSVWRQAPGKGLEWVSVISGKTDGSGST 189
QY 59 YYSDSVKGKFTTISRDNKNTLYLQWMSLRADSAVYFCTRVLTGT-----YYFDSM 109
DB 190 YYADSVKGRFTTISRDNKNTLYLQWMSLRADTAIVYICARGXGKXSLSGXYYYHYHFDYW 249
QY 110 GGGTLTVSS 119
DB 250 GGGTLTVSS 259
RESULT 29
US-09-956-087-3
; Sequence 3, Application US/09956087
; Patent No. US20020161201A1
; GENERAL INFORMATION:
APPLICANT: Filipula, David R.

APPLICANT: FILIPULA, DAVID
MANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-087-3
Query Match 77.8%; Score 485.5; DB 9; Length 263;
Best Local Similarity 73.8%; Pred. No. 5.8e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;
QY 1 EVQLVDSGGDFVQPGGSLRLVSCAASGFAFSHYAMSVWRQAPGKGLEWVAIIS--SGSGST 58
DB 130 EVQLVDSGGGLVQPGGSLRLSLCAASGFTFSYAMSVWRQAPGKGLEWVSVISGKTDGSGST 189
QY 59 YYSDSVKGKFTTISRDNKNTLYLQWMSLRADSAVYFCTRVLTGT-----YYFDSM 109
DB 190 YYADSVKGRFTTISRDNKNTLYLQWMSLRADTAIVYICARGXGKXSLSGXYYYHYHFDYW 249
QY 110 GGGTLTVSS 119
DB 250 GGGTLTVSS 259
RESULT 30
US-09-983-580-6
; Sequence 6, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
APPLICANT: Filipula, David R.

APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. US20020151061a1el Method for Targeted Delivery of Nucleic Acid
FILE REFERENCE: 0977.2300002
CURRENT APPLICATION NUMBER: US/09/983.580
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
US-09-983-580-6

Query Match 77.8%; Score 485.5; DB 9; Length 283;
Best Local Similarity 73.8%; Pred. No. 6.3e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFHYAMSWVRQAPGKGLWVAYIS--SGSGGT 58
DB 130 EVOLVESGGGLVPGGSLRVSCAAGFTTSSVAMSWVRQAPGKGLWVAYISGKTDGGST 189
QY 59 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLT-----YFPDSW 109
DB 190 YVADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCAKGRGXSLSGXYHYHFDYW 249
QY 110 GGGTLTVSS 119
DB 250 GGGTLTVSS 259

RESULT 31
US-09-985-442-6
Sequence 6, Application US/09985442
Patent No. US20020156248A1
GENERAL INFORMATION:
APPLICANT: Filipula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. US20020156248A1el Method for Targeted Delivery of Nucleic Acid
FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985.442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
NAME/KEY: UNSURE

LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
US-09-985-442-6

Query Match 77.8%; Score 485.5; DB 9; Length 283;
Best Local Similarity 73.8%; Pred. No. 6.3e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFHYAMSWVRQAPGKGLWVAYIS--SGSGGT 58
DB 130 EVOLVESGGGLVPGGSLRVSCAAGFTTSSVAMSWVRQAPGKGLWVAYISGKTDGGST 189
QY 59 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLT-----YFPDSW 109
DB 190 YVADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCAKGRGXSLSGXYHYHFDYW 249
QY 110 GGGTLTVSS 119
DB 250 GGGTLTVSS 259

RESULT 32
US-09-840-459-82
Sequence 82, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran H.
APPLICANT: O'Brien, Stobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840.459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 82
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-82

Query Match 77.7%; Score 485; DB 9; Length 123;
Best Local Similarity 76.4%; Pred. No. 3e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFHYAMSWVRQAPGKGLWVAYISGSGGT 60
DB 1 EVOLVESGGGLVPGGSLRVSCAAGFTTSSVAMSWVRQAPGKGLWVAYISGSGGT 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLT-----YKGTYYFDSWGGLT 116
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCAKGRGXSLSGXYHYHFDYW 120
QY 117 VSS 119

```
Db          121 VSS 123

RESULT 33
US-10-766-773-82
; Sequence 82, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: Lakosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-766-773-82

Query Match          77.7%; Score 485; DB 16; Length 123;
Best Local Similarity 76.4%; Pred. No. 3e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

QY      1 EVOLVESGDDFVOPGSLRVSCAASGAFAPSHYAMSVWRQAPGKLEWVAIISGSGTYY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVOLLESGGGLVOPGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAISGSGYTTY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 SDSVKRFTISRDNKNTLYLQWRSIRAPDSAVYFCTR----VKLGTYYPDSWGQGTLLT 116
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKRFTISRDNKNTLYLQWNSIRAPDVAIVYCAKKRPGDYSGSYLDYWGQGTLLVT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      117 VSS 119
        |||
Db      121 VSS 123

RESULT 34
US-10-766-610-82
; Sequence 82, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: Lakosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Stobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
```

```
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-766-610-82

Query Match          77.7%; Score 485; DB 16; Length 123;
Best Local Similarity 76.4%; Pred. No. 3e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

QY      1 EVOLVESGDDFVOPGSLRVSCAASGAFAPSHYAMSVWRQAPGKLEWVAIISGSGTYY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVOLLESGGGLVOPGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAISGSGYTTY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 SDSVKRFTISRDNKNTLYLQWRSIRAPDSAVYFCTR----VKLGTYYPDSWGQGTLLT 116
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKRFTISRDNKNTLYLQWNSIRAPDVAIVYCAKKRPGDYSGSYLDYWGQGTLLVT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      117 VSS 119
        |||
Db      121 VSS 123

RESULT 35
US-10-733-563-82
; Sequence 82, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-563-82

Query Match          77.7%; Score 485; DB 16; Length 123;
Best Local Similarity 76.4%; Pred. No. 3e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

QY      1 EVOLVESGDDFVOPGSLRVSCAASGAFAPSHYAMSVWRQAPGKLEWVAIISGSGTYY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVOLLESGGGLVOPGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAISGSGYTTY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 SDSVKRFTISRDNKNTLYLQWRSIRAPDSAVYFCTR----VKLGTYYPDSWGQGTLLT 116
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKRFTISRDNKNTLYLQWNSIRAPDVAIVYCAKKRPGDYSGSYLDYWGQGTLLVT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      117 VSS 119
        |||
Db      121 VSS 123

RESULT 36
US-09-880-748-1421
```

```
; Sequence 1421, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
; FILE REFERENCE: PF533
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1421
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1421
```

```
Query Match 77.7%; Score 485; DB 10; Length 248;
Best Local Similarity 76.8%; Pred. No. 6,1e-36;
Matches 96; Conservative 8; Mismatches 15; Indels 6; Gaps 2;
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```
QY 1 EVOLVESGDDFVPGGSLRVSCAAGFAPSHYAMSVWRQAPGKLEWVAYISGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSIARSDAVYFCTRVKLT-----VKLG-TYYPDSWGQTL 114
DB 61 ADSVKRFTISRDNKNTLYLQWRSIARSDAVYFCTRVKLT-----VKLG-TYYPDSWGQTL 120
QY 115 LVVSS 119
DB 121 VVVSS 125
```

```
RESULT 37
US-10-293-418-1421
; Sequence 1421, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1421
; LENGTH: 248
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-293-418-1421
```

```
Query Match: 77.7%; Score 485; DB 14; Length 248;
Best Local Similarity 76.8%; Pred. No. 6,1e-36;
Matches 96; Conservative 8; Mismatches 15; Indels 6; Gaps 2;
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```
QY 1 EVOLVESGDDFVPGGSLRVSCAAGFAPSHYAMSVWRQAPGKLEWVAYISGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSIARSDAVYFCTRVKLT-----VKLG-TYYPDSWGQTL 114
DB 61 ADSVKRFTISRDNKNTLYLQWRSIARSDAVYFCTRVKLT-----VKLG-TYYPDSWGQTL 120
QY 115 LVVSS 119
DB 121 VVVSS 125
```

```
RESULT 38
US-10-800-197-15
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```
; Sequence 15, Application US/10800197
; Publication No. US20040202655A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Morton, Philip A et al.
; TITLE OF INVENTION: ANTIBODIES TO IGF-1 RECEPTOR FOR THE TREATMENT OF CANCERS
; FILE REFERENCE: 01343/1
; CURRENT APPLICATION NUMBER: US/10/800,197
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/455,094
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 15
; LENGTH: 251
; TYPE: PRT
; ORGANISM: artificial
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```
; FEATURE:
; OTHER INFORMATION: phage display generated antibody
US-10-800-197-15
```

```
Query Match 77.7%; Score 485; DB 17; Length 251;
Best Local Similarity 75.6%; Pred. No. 6,2e-36;
Matches 93; Conservative 10; Mismatches 16; Indels 4; Gaps 1;
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```
QY 1 EVOLVESGDDFVPGGSLRVSCAAGFAPSHYAMSVWRQAPGKLEWVAYISGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSIARSDAVYFCTRVKLT-----GTYFDSWGQTL 116
DB 61 ADSVKRFTISRDNKNTLYLQWRSIARSDAVYFCTRVKLT-----GTYFDSWGQTL 120
QY 117 VSS 119
DB 121 VSS 123
```

```
RESULT 39
US-10-474-832-68
; Sequence 68, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
```

; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 68
 ; LENGTH: 118
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: polypeptide
 US-10-474-832-68

Query Match 77.6%; Score 484.5; DB 15; Length 118;
 Best Local Similarity 81.5%; Pred. No. 3.2e-36;
 Matches 97; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVGLVESGGDFVQPGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60
 DB 1 EVGLVESGGGLVQPGSLRVSCAAGFTFSRYTMSWVRQAPGKLEWVATISSGGH-TTY 59
 QY 61 SDSVKGRFTISRDNSTKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
 DB 60 LDSVKGRFTISRDNSTKNTLYLQMNLSLRAEDTAVYCTRGFDGSGYFDVWGQGTLLTVSS 118

RESULT 40
 US-10-474-832-69
 ; Sequence 69, Application US/10474832
 ; Publication No. US20040081651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BIOGEN, INC.
 ; TITLE OF INVENTION: ANTIBODIES TO VLA-1
 ; FILE REFERENCE: A101 PCT
 ; CURRENT APPLICATION NUMBER: US/10/474,832
 ; CURRENT FILING DATE: 2003-10-14
 ; PRIOR APPLICATION NUMBER: 60/283,794
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/303,689
 ; PRIOR FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 69
 ; LENGTH: 118
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: polypeptide
 US-10-474-832-69

Query Match 77.6%; Score 484.5; DB 15; Length 118;
 Best Local Similarity 81.5%; Pred. No. 3.2e-36;
 Matches 97; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVGLVESGGDFVQPGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60
 DB 1 EVGLVESGGGLVQPGSLRVSCAAGFTFSRYTMSWVRQAPGKLEWVATISSGGH-TTY 59
 QY 61 SDSVKGRFTISRDNSTKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
 DB 60 LDSVKGRFTISRDNSTKNTLYLQMNLSLRAEDTAVYCTRGFDGSGYFDVWGQGTLLTVSS 118

Search completed: December 17, 2004, 18:38:03
 Job time : 230.978 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:11:22 ; Search time 46.7978 Seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-9

Perfect score: 624
Sequence: 1 EVQLVESGGDFVQPGSLRV.....KLGTYYFDSWGQGTLLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	80.3	139	2 S31107	IG heavy chain - h
2	501	80.3	139	2 S31666	IG heavy chain V r
3	486	77.9	119	2 D36005	IG heavy chain V r
4	484	77.6	119	2 S31108	IG heavy chain V r
5	483	77.4	140	2 S31686	IG heavy chain - h
6	482.5	77.3	140	2 S70442	IG heavy chain pre
7	480	76.9	123	2 S31114	IG heavy chain - h
8	479	76.8	125	2 S30531	IG heavy chain V r
9	477.5	76.5	124	2 S20782	IG heavy chain V r
10	477.5	76.5	128	2 S26790	IG heavy chain V r
11	474	76.0	119	2 C36005	IG heavy chain V r
12	474	76.0	135	2 S31598	IG heavy chain V r
13	473.5	75.9	120	2 S48798	IG heavy chain V r
14	473.5	75.9	120	2 S48798	IG heavy chain V r
15	471	75.5	160	2 S05271	IG heavy chain pre
16	470.5	75.4	118	2 S31105	IG heavy chain (bu
17	470.5	75.4	135	2 I37778	IG variable region
18	470	75.3	119	2 F36005	IG heavy chain V r
19	469.5	75.2	120	2 S44111	IG heavy chain V-D
20	469	75.2	127	2 S38489	IG heavy chain - h
21	466.5	74.8	122	2 PC2398	anti-tetanus toxin
22	466	74.7	121	2 G36005	IG heavy chain V r
23	466	74.7	132	2 S31603	IG heavy chain V r
24	466	74.7	133	2 S23624	IG heavy chain V r
25	465	74.5	134	2 S31679	IG heavy chain V r
26	464.5	74.4	139	2 S31674	IG heavy chain V r
27	464	74.4	121	2 I55673	IG heavy chain - h
28	464	74.4	121	2 S19666	IG heavy chain V r
29	464	74.4	134	2 S31699	IG heavy chain V r

30	463.5	74.3	114	2 S31120	IG heavy chain - h
31	463.5	74.3	147	2 I37780	IG variable region
32	462.5	74.1	128	2 S26786	IG heavy chain V r
33	462	74.0	139	2 I37781	IG variable region
34	461.5	74.0	136	2 S31587	IG heavy chain V r
35	461.5	74.0	137	2 S78054	IG heavy chain pre
36	459.5	73.6	114	2 S46390	IG heavy chain V r
37	459	73.6	140	2 A30532	IG heavy chain pre
38	458.5	73.5	141	2 S31669	IG heavy chain V r
39	457.5	73.3	122	2 E36005	IG heavy chain V r
40	457	73.2	123	2 S26794	IG heavy chain V r
41	455	72.9	119	2 B34353	anti-peptide Fab'
42	454.5	72.8	120	2 S31112	IG heavy chain - h
43	453.5	72.7	118	2 S31116	IG heavy chain - h
44	453.5	72.7	122	2 S20772	IG heavy chain V r
45	453.5	72.7	133	2 S31510	IG heavy chain - h

ALIGNMENTS

RESULT 1

S31107
IG heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31107
R/Rapporteur, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; M0ID:92111633; PMID:1730252
A/Accession: S31107
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RA>
A/Cross-references: EMBL:X62955
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 501; DB 2; Length 119;
Best Local Similarity 79.8%; Pred. No. 3,7e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGSLRVSCAAGFAPSHVMSVWROAPGKLEWVAIYSGSGSTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSSVAMSWROAPGKLEWVAIYSGSGSTYY 60
QY 61 SDSVKGRFTISRDNSKNTLYLQWRSIPRARDSDAVYFCTRVYLGTYFDSWGQGTLLTVSS 119
DB 61 ADSVKRFTISRDNSKNTLYLQWNSLRARDTAVYCAKPGASVYFDYWGQGTLLTVSS 119

RESULT 2

S31666
IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31666
R/Cultivator, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31666
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-138 <CUI>
A/Cross-references: EMBL:Z14202; NID:930963; PIDN:CAA78571.1; PID:930964
C/Keywords: heterotetramer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

```
Query Match 80.3%; Score 501; DB 2; Length 138;
Best Local Similarity 78.2%; Pred. No. 4.3e-38;
Matches 93; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVOPGSLRVSCAASGAFPSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
DB 20 EVQLTSGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGSGSTYY 79
QY 61 SDVKGKFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFPSMGQGTLLTVSS 119
DB 80 ADSVKGKFTISRDNKNTLYLQMRSLRAEDTAIVYCAKAKRTGYTFPLMGRGTLTVYSS 138

RESULT 3
D36005
Ig heavy chain V region (M43) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: D36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: D36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
C/Genetics:
A/Cross-references: GB:M34024
A:Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin heavy chain variable gene
C/Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 486; DB 2; Length 119;
Best Local Similarity 77.3%; Pred. No. 8.2e-37;
Matches 92; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVOPGSLRVSCAASGAFPSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
DB 1 EVQLTSGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
QY 61 SDVKGKFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFPSMGQGTLLTVSS 119
DB 61 ADSVKGKFTISRDNKNTLYLQMRSLRAEDTAIVYCAKAKMDNDWFPDWGQGTLLTVSS 119

RESULT 4
S31108
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31108
R/Raapportet, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31108
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RAA>
A/Cross-references: EMBL:X62956
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 484; DB 2; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.2e-35;
Matches 93; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGDFVOPGSLRVSCAASGAFPSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
DB 1 EVQLTSGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
QY 61 SDVKGKFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFPSMGQGTLLTVSS 119
DB 61 ADSVKGKFTISRDNKNTLYLQMRSLRAEDTAIVYCAKAKRRLTGTDPYMGQGTLLTVSS 119

RESULT 5
S31686
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31686
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31686
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
A/Cross-references: EMBL:Z14205; NID:930969; PIDN:CAA78574.1; PID:930970
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 483; DB 2; Length 140;
Best Local Similarity 77.7%; Pred. No. 1.8e-36;
Matches 94; Conservative 8; Mismatches 17; Indels 2; Gaps 1;
```

```
QY 1 EVOLVESGDFVOPGSLRVSCAASGAFPSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
DB 20 EVQLTSGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGSGSTYY 79
QY 61 SDVKGKFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFPSMGQGTLLTVSS 118
DB 80 SDVKGKFTISRDNKNTLYLQMRSLRAEDTAIVYCAKCPAGSGSPFDYWGQGTLLTVSS 139

QY 119 S 119
DB 140 S 140

RESULT 6
S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: S70442
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fet
A/Reference number: S70442; MUID:93024508; PMID:183695
A/Accession: S70442
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
A/Cross-references: UNIPROT:Q8WUK1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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```
Query Match 77.3%; Score 482.5; DB 2; Length 140;
Best Local Similarity 77.5%; Pred. No. 2e-36;
Matches 93; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVOPGSLRVSCAASGAFPSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
DB 20 EVQLTSGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYRDGSKY 79
QY 61 SDVKGKFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFPSMGQGTLLTVSS 119
DB 61 SDVKGKFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFPSMGQGTLLTVSS 119
```

Db 80 ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCARDHIVGATYFDYWGQGLTVTVSS 139

RESULT 7

S31114

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31114

R/Martini, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurmat

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line VH3 genes and short diverse third complement

A/Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31114

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-123 <RA>

A/Cross-references: EMBL:X62963

C/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 480; DB 2; Length 123;

Best Local Similarity 75.6%; Pred. No. 2.9e-36;

Matches 93; Conservative 9; Mismatches 17; Indels 4; Gaps 1;

Db 1 EVOLVESGDFVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWVAYISSGSGTYY 60

1 EVOLVESGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSISSGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCTRVKLG---TYFDSWGQGLTL 116

Db 61 ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCAKASLYLRFLEMLFDYWGQGLTV 120

QY 117 VSS 119

Db 121 VSS 123

RESULT 8

S30531

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: S30531

R/Martini, X.

Submitted to the EMBL Data Library, October 1992

A/Reference number: S30520

A/Accession: S30531

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-125 <MAR>

A/Cross-references: UNIPROT:Q9UL91; EMBL:Z18317

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 479; DB 2; Length 125;

Best Local Similarity 72.8%; Pred. No. 3.7e-36;

Matches 91; Conservative 14; Mismatches 14; Indels 6; Gaps 1;

Db 1 EVOLVESGDFVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWVAYISSGSGTYY 60

1 EVOLVESGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSISSSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCTRVK-----LGYTFDSWGQGL 114

Db 61 ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCARSRNRYSSGYSHYFDYWGQGL 120

RESULT 9

S20782

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C/Accession: S20782

R/Martini, F.; Wang, J.; Schroeder, H.W.

submitted to the EMBL Data Library, April 1992

A/Description: Analysis of the Igh and Igg rearranged VH repertoire of human cord blood

A/Reference number: S20765

A/Accession: S20782

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-124 <MOR>

A/Cross-references: EMBL:Z11946; NID:G33897; PIDN:CAA78003.1; PID:G33898

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 477.5; DB 2; Length 124;

Best Local Similarity 72.6%; Pred. No. 5e-36;

Matches 90; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

Db 1 EVOLVESGDFVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWVAYISSGSGTYY 60

1 EVOLVESGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSISSGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCTRVKLGTY-----YFDSWGQGLTL 115

Db 61 ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCAKRIALFGVVIPIFDYWGQGLTV 120

QY 116 TVSS 119

Db 121 TVSS 124

RESULT 10

S26790

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C/Accession: S26790

R/Martini, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam1)

A/Reference number: S26786; MUID:92111632; PMID:1730251

A/Accession: S26790

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-128 <MOR>

A/Cross-references: EMBL:X61013; NID:G32798; PIDN:CAA43347.1; PID:G1335128

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 477.5; DB 2; Length 128;

Best Local Similarity 71.1%; Pred. No. 5.1e-36;

Matches 91; Conservative 13; Mismatches 15; Indels 9; Gaps 1;

Db 1 EVOLVESGDFVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWVAYISSGSGTYY 60

1 EVOLVESGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSISSSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCTRVK-----VKLGYTFDSWGQ 111

Db 61 ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCARPGGGLRIAAVAGDWYFDLWGR 120

QY 112 GTLLTVSS 119

Db 121 GTLLTVSS 128

RESULT 11

Ig heavy chain V region (30pt) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C/Accession: C36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: C36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: GB:M18513
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: Immunoglobulin homology <IIM>

Query Match	76.0%	Score 474	DB 2	Length 119
Best Local	77.3%	Pred. No. 9	8e-36	
Matches 92	Conservative	8	Mismatches 19	Indels 0
			Gaps	0

Oy

1 EVQLVESGGDVPQPGGSLRVSCLASGFASHYMSWRAPGKLEWVAIISGGSGSTYY 600
|||:||| |||||:|||||:|||||: |||
|||:||| |||||:|||||:|||||: |||

Db

1 EVQLVESGGGVLPGGSLRLTSCASGFTFSSSYNMSWVRQAPEGLEWVSAISGSGSSTYY 600

```
QY 61 SDSVGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRKYLGTYFDSWGQGLTVSS 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKADAGWGSGFDYWGQGLTVTVSS 119
```

RESULT 12

Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31598
R/Cuistler, A.M.; Gauthier, L.; Boubil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31598
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-135 <EBL>
A/Cross-references: EMBL:214170; NID:g31001; PIDN:CAA78539.1; PID:g31002
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
E/31-114/Domain: immunoglobulin homology <1MM>

Query Match	76.0%	Score 474	DB 2	Length 135
Best Local Similarity	75.6%	Pred. No. 1.1e-35		
Matches 90	Conservative 9	Mismatches 20	Indels 0	Gaps 0

OY 1 EVQLVESGGDFAVQPGGSLRVSCASGFARSHYAMSWVRQAPEGKLEWVAITYSSGGSGTYY 600
:
Dd 17 QVQLVESGGGVQPGRGLRLTSCASGFPTSSYGMMHWRQAPEGKEWVAFIKYDSNKKY 760

```
QY      61 SDSVAGRFTISRDNASKNTLYLQMRSLRAEDSAVYFCTRYKLGTYFFDSWGQGLTVSS 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      77 ADSVAGRFTISRDNASKNTLYLQNNSLRAEDTAVYCAKLSWEVSRFDYWGQGLTVYSS 135
```

RESULT 13

Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1995
 C/Accession: S31588
 R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992

A,Description:Mechanisms that generate human immunoglobulin diversity operate from the
A,Reference number: S31585
A,Accession: S31588
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-140 < EBI>
A,Cross-references: KUBI,Z14200; NID:G30957; PIDN:CAA78569.1; PID:G30958
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
I,34-117/Domain: immunoglobulin homology <IMM>

Query Match Similarity	76.0%	Score 474; DB 2;	length 140;
Best Local Similarity	76.9%	Pred. No. 1.2e-35;	
Matches 93; Conservative	9;	Mismatches 17;	Indels 2; Gaps 2

```
Oy      1 EVQLVESGGD FVQPGSSLRVSCAASGAFSHYAMSWRQA PGKLEWVA YISSGSSTYY 60
        |||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      20 EVGLTSGGGL VQPGSLRLSCAASGTFSSYAMSWRQA PGKLEWVA ISIGSGSTYY 79
```

```

61 SDSVKGKRFISRDNSKNTLYLQMSLRRAEDSAVVFCTR-VKLGT-YFDSWGQGLTLTVS 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
80 ADSVKGKRFISRDNSKNTLYLQMSLRRAEDTAVVYCAKHHDYSNYIFDYWGQGLTLTVS 139

```

QY	119 S	119
Db	140 S	140

RESULT 14

Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C/Accession: S48798
 R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A/Description: Molecular characterization of natural human anti-Sm autoantibodies
 A/Reference number: S48797
 A/Accession: S48798
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-120 <EMBL>
 A/Cross-references: EMBL:246382; NID:9562324; PIDN:CAA6521.1; PID:q1340167
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 C/15-98/Domain: immunoglobulin homology <IMM>

Query Match	75.9%	Score 473.5	DB 2	Length 120
Best Local Similarity	76.7%	Pred. No. 1.1e-35		
Matches 92	Conservative 10	Mismatches 17	Indels 1	Gaps 1

Oy

1 EVQLVESGGGFVDPGSSLRVSCAASGAFAFSHYAMSWVRQAPGKLEWVAIISGGSGSTYY 600
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Db

1 EVQLLESGGGLVQPGSLRLTSCAASGTFSSYAMSWVRQAAPGKLEWVASAISGGSGSTYY 600

```

Oy      61 SDSYKGRFTISRDNKNTLYLQMSLRAEASAVVFCTRVK-LGTYFPDSWGCGTLVYSS 113
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSYKGRFTISRDNKNTLYLQMSLRAEADTAVVYCAKDRGFWSGYKDYWGCGTLVYVSS 120

```

RESULT 15

Ig heavy chain precursor - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1992 #sequence _revision 30-Jun-1992 #text change 09-Jul-2004
 C/Accession: S05271; S04602
 R/Kishimoto, T.
 submitted to the EMBL Data Library, March 1989
 A/Reference number: S05270
 A/Accession: S05271
 A/Molecule type: mRNA
 A/Residues: 1-160 <K1S1>
 A/Cross-references: UNIPROT:Q96BB9, EMBL:X14584

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <HAM>
A:Cross-references: EMBL:Z31387; NID:g947965; PIDN:CAH8362.1; PID:g940522
C:Superfamily: immunoglobulin V' region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	75.2%;	Score 469.5;	DB 2;	length 120;
Best Local Similarity	75.0%;	Pred. No. 2.5e-35;		
Matches 90;	Conservative 10;	Mismatches 19;	Indels 1;	Gaps 1

[illegible]

RESULT 20

538489

ig heavy chain - human (irrigament)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R:Markers: J.D.; Quehenand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993

```

;Reference number: S38488
;Accession: S38489
;Status: preliminary
;Molecule type: DNA
;Residues: 1-127 <MAR>
;Cross-references: EMBL:E23028; NID:g414025; PION:CAA80563.1; PID:g414026
;superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotrimer; immunoglobulin
;15-98/Domain: immunoglobulin homology <IMM>

Query Match          75.2%; Score 469; DB 2; Length 127;
Best Local Similarity 71.7%; Pred. No.2.9e-35;
Matches 91; Conservative 9; Mismatches 17; Indels 10; Gaps 1

```

```

QY 1 EVOLVESGGDPVQVQGGSLRVSCAASGPAFASHYAMSWVQAPEKGLIEWALYISSGSGSTYY 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 QVQLVQSGGYYVQVQGGSLRLCSAASGFTFSASMSWVQAPEKGLIEWALSISGSGSTYY 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 61 SDSVKGKFTISRDNASKNTLYIQMSLRADDAVYFCYTV-----KIGTYIFDSWG 110
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 ADSVKGKFTISRDNASKNTLYIQMNSLRADDAVYCAKEGPPASDYDSSGYSFDYWG 120
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 111 QGTLTV 117
   |||::|||
Db 121 QGTLTV 127

```

RESULT 21
PC2398

anti-tetanus toxin 9F12 Fab heavy-chain - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 23-May-1997
C/Accession: PC2398
R/Expositor: G.; Scarcelll, E.; Traboni, C.
Gene 148, 167-168, 1994
Title: Phase display of a human antibody against Clostridium tetani toxin

F:31-35/Region:	complementarity determining region 1
F:50-66/Region:	complementarity determining region 2
Query Match	74.8%; Score 466.5; DB 2; Length 122;
Best Local Similarity	73.8%; Pred. No. 4.7e-35;
Matches 90; Conservative 12; Mismatches 17; Indels 3; Gaps 1.	

```

QY      1 EVOLVESGGDFFVQPGGSLRVSCAASGFAPFSHYAMSWROAPGKLEWVAATSSGSGSTYY 60
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 EVOLVQSGGGGLVQPGGSVRLSCAASGFSFSSYAMSWROAPGMKLEWVAATISARGITTTY 60

QY      61 SDPSVKRPFISHDNSKNTLYIQMRSLRAEDSAVVEFCTRVK---LGTYYPDPSWGGTLLTV 117
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 AASVTRGLTISKDNSMNTLYLHNSLRADPDATVYVCAKAGKQMLAHYTFDPSWGGTLLTV 120

QY      118 SS 119
      ||
Db      121 SS 122

```

RESULT 22

G36005

IG heavy chain region (M/4) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #next_change 09-Jul-2004
C:Accession: G36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene segments in the human IgG1 heavy chain region
#:Reference number: A36005; NUID:90349571; PMID:211773

```

n/Reason:0n.138503
A;/Status: preliminary
A;/Molecule type: mRNA
A;/Residues: 1-121 <SCH>
A;/Cross-references: UNIPROT:Q8WUK1; GB:M34031
C;/Genetics:
A;/Gene: GDB:IGH@; IGHDI1
A;/Cross-references: GDB:118731; OMIM:146910
A;/Map position: 14q32.33-14q32.33
C;/Superfamily: Immunoglobulin V region; immunoglobulin
C;/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      74.7%   Score 466;   DB 2;   Length 121;
Best Local Similarity 76.9%;   Pred. No. 5.2e-35;
Matches 93;   Conservative 7;   Mismatches 19;   Indels 2;   Gaps 1

```

QY	1	EVOLVESGCDPFQPGGSLRVSCAASGFNFHSYAAASWROAPGKLEWAAVSISSGSETTY	60
QY	:		:
Db	1	QVQLVESGGGVQPPRSIRLRISCAASGFFPSSSYAAHWROAPGKLEWAAVSIYDGSNKYY	60
QY	61	SSSVKGRFTISRDNSKNTLYIQOMSLRAEDSAYVECTRVK--LGITYYFDSMGQOTLLTVS	118
QY	:		:
Db	61	ASISVKGKFTISRDNSKNTLYIQOMSLRAEDRAVYYICARDRDNMGMALFDYMGGCLTVTVS	120
QY	119	S	119
QY	121	S	121

RESULT 23

S31603

Ig heavy chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Mar-1994 #sequence 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31603
 R/Cuisinier, A.M.; Gauchier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992


```

Oy 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVVFCTV--KLGTYYPDMSGQGLTLTVS 118
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTTISRDNKNTLYLQMRSLRAEDTAIVYCAAPRPAASPPYIDWGQGLTLTVS 120

Oy 119 S 119
      |
Db 121 S 121

RESULT 28
S19666
Ig heavy chain V region (VH3DJH4) - human
C|Species: Homo sapiens (man)
C|Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C|Accession: S19666
R|Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter
J.; Mol. Biol. 222, 581-597, 1991
A|Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A|Reference number: S19663; MUID:92085276; PMID:1748994
A|Accession: S19666
A|Molecule type: mRNA
A|Residues: 1-121 <MAR>
A|Cross-references: EMBL:X61646; NID:g37688; PIDD:CAA43827.1; PID:g1335369
C|Superfamily: immunoglobulin V region; immunoglobulin homology
C|Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 464; DB 2; Length 121;
Best Local Similarity 76.0%; Pred. No. 7.9e-35;
Matches 92; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

Oy 1 EVOLVESGDDPVQPGSLRVSCAASGFAFSHYAMSWVQAQPGKLEWVAIYSSGSGSTYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGGAVQPGSRSLRSCAASGFTFSSYGMMWVQAQPGKLEWVAIYSDGSNKYY 60

Oy 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVVFCT--TRVYLGTYFPDMSGQGLTLTVS 118
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTTISRDNKNTLYLQMRSLRAEDTAIVYCAATGYSNGMGTIDYWGQGLTLTVS 120

Oy 119 S 119
      |
Db 121 S 121

RESULT 29
S31699
Ig heavy chain V region - human (fragment)
C|Species: Homo sapiens (man)
C|Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C|Accession: S31699
R|Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A|Description: Mechanisms that generate human immunoglobulin diversity operate from the
A|Reference number: S31585
A|Accession: S31699
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-134 <CUR>
A|Cross-references: EMBL:Z14201; NID:g30961; PIDD:CAA76570.1; PID:g30962
C|Superfamily: immunoglobulin V region; immunoglobulin homology
C|Keywords: heterotetramer; immunoglobulin
P:34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 464; DB 2; Length 134;
Best Local Similarity 76.5%; Pred. No. 8.8e-35;
Matches 91; Conservative 7; Mismatches 17; Indels 4; Gaps 1;

Oy 1 EVOLVESGDDPVQPGSLRVSCAASGFAFSHYAMSWVQAQPGKLEWVAIYSSGSGSTYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGVVHPGSGRLSCAASGFTFSSYAMSWVQAQPGKLEWVAISGSGSTYY 79

Oy 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVVFCTVYKLGTYFPDMSGQGLTLTVS 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```
DB      80 SDSVKGRLTISDNRKNTLYLQMSLRADDTAVYYCARRR-----DLDPYWGQTGLTVSS    134

RESULT 30
S31120
Ig heavy chain - human
C|Species: Homo sapiens (man)
C|Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C|Accession: S31120
R|Raphoport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, B.R. J. Immunol. 22, 247-251, 1992
A>Title: Restricted utilization of germ-line VH3 genes and short diverse third complement A;Reference number: S31104; WUID:92111633; PMID:1730252
A|Accession: S31120
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A|Molecule type: mRNA
A|Residues: 1-114 <RAA>
A|Cross-references: EMBL:X62972
A|Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C|Superfamily: immunoglobulin V region; immunoglobulin homology
C|Keywords: heterotrimer; immunoglobulin
F.15-98/Domain: immunoglobulin homology <IMM>

Query Match          74.3%; Score 463.5; DB 2; Length 114;
Best Local Similarity 74.8%; Pred. No. 8.2e+35;
Matches             89; Conservative 12; Mismatches 13; Indels 5; Gaps 1;

OY      1 EVQLVESGGDFYPGSGSLRVSCAASGFARFSHYAMSVWRQAPGKGLEWVAIISGSGSTTY    60
        :|||:::||:::||:::||::||::||::||::||::||::||::||::||::||::||
DB       1 QVALVESGGGLYKPGGSILRLSCAASGFTPSDYMSIRQAPEGLEWVSIISSGSTITY    60
        |||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      61 SDVKGRPTISDNSKNITLYLMRSIRADSANYPCTRYKLGYTPDSWKQGTLITVSS    119
        :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB       61 ADSVGKRPFTISRDNKNSLTYLQMNSLRADDTAVYYC-----ASNFDYWQGITLVTVSS    114
        |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 31
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C|Species: Homo sapiens (man)
C|Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C|Accession: I37780; S25474
R|Denaison, C.; Chastagner, P.; Therez, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A>Title: Somatic diversification in the heavy chain variable region genes expressed by hA;Reference number: A36876; WUID:94119917; PMID:8390556
A|Accession: I37780
A>Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-147 <RES>
A|Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
C|Superfamily: immunoglobulin V region; immunoglobulin homology
F.28-111/Domain: immunoglobulin homology <IMM>

Query Match          74.3%; Score 463.5; DB 2; Length 147;
Best Local Similarity 75.0%; Pred. No. 1.1e+34;
Matches            93; Conservative 7; Mismatches 19; Indels 5; Gaps 2;

OY      1 EVQLVESGGDFYPGSGSLRVSCAASGFARFSHYAMSVWRQAPGKGLEWVAIISGSGSTTY    60
        :|||:::||:::||:::||::||::||::||::||::||::||::||::||::||
DB       14 EVQLVESGGGLVQPFGSLRLSCAASGFTISSYSMSVRQRAPGKGLEWNAIKDGSEKTY    73
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      61 SDVKGRPTISDNSKNITLYLMRSIRADSANYPCTR--VKLGTYFP---DSWGQGTLL    115
        :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB       74 ADSVGKRPFTISRDNKNTLYLQNNSLRADDTAVYYCAKDGEGLVYYYGMGVGCGTTV    133
        |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      116 TVSS    119
        ||||
DB     134 TVSS    137
```

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_rev: 13-Jan-1995 #text_change: 20-Jun-2000

C/Accession: S26786

R/Moritz, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family

A/Reference number: S26786; MUID:92111632; PMID:1730251

A/Accession: S26786

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-128 <MOR>

A/Cross-references: EMBL:X61014; NID:932800; PIDN:CAA43348.1; PID:9135129

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 462.5; DB 2; Length 128;

Best Local Similarity 69.5%; Pred. No. 1.1e-34;

Matches 91; Conservative 12; Mismatches 13; Indels 15; Gaps 2;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKGLWVAYISGGSGTYY 60

1 QVQVSGGGGLVPGGSLRVSCAASGFTSDYTMWIRAPGKGLWVAYISSSSTYNY 60

1 SDVSKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFDS 108

1 ADVSKRFTISRDNKNTLYLQNRSLRAEDTAVYYCAR---GLYCSSTSCYINSMWFD 117

109 WGGGTLTVSS 119

118 WGGGTLTVSS 128

RESULT 33

137781 Ig variable region (VDJ) (clone T21-9) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence_rev: 16-Feb-1996 #text_change: 23-Jul-1999

C/Accession: I37781; S25475

R/Demaison, C.; Chateigner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A/Title: Somatic diversification in the heavy chain variable region genes expressed by h

A/Reference number: A36876; MUID:94119917; PMID:8290556

A/Accession: I37781

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-139 <RES>

A/Cross-references: EMBL:X67908; NID:933580; PIDN:CAA48106.1; PID:913581

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

F/35-118/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 462; DB 2; Length 139;

Best Local Similarity 74.8%; Pred. No. 1.4e-34;

Matches 89; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKGLWVAYISGGSGTYY 60

21 EVOLVSGGGGLVPGGSLRVSCAASGFTSSYMSWVROAPGKGLWVAINIKODGSEKTY 80

61 SDVSKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGGTLLTVSS 119

81 VDSVKRFTISRDNKNTLYLQNRSLRAEDTAVYYCARKAKGAKAFIMWGGTMTVTVSS 139

RESULT 34

S31587 Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_rev: 10-Nov-1995 #text_change: 23-Jul-1999

C/Accession: S31587

R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31587

A/Accession: S31587

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-136 <CUI>

A/Cross-references: EMBL:Z14189; NID:931005; PIDN:CAA78558.1; PID:911006

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/31-114/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 461.5; DB 2; Length 136;

Best Local Similarity 76.7%; Pred. No. 1.5e-34;

Matches 92; Conservative 7; Mismatches 20; Indels 1; Gaps 1;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKGLWVAYISGGSGTYY 60

17 EVOLVSGGGGLVPGGSLRVSCAASGFTSSYMSWVROAPGKGLWVAINIKODGSEKTY 76

61 SDVSKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGGTLLTVSS 119

77 VDSVKRFTISRDNKNTLYLQNRSLRAEDTAVYYCARGLTGATDAFDLWGGTMTVTVSS 136

RESULT 35

S78054

Ig heavy chain precursor V-D-J region (clone mAb 60VH) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_rev: 05-Dec-1997 #text_change: 23-Jul-1999

C/Accession: S78054; S23719

R/Harindranath, N.

submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78054

A/Molecule type: mRNA

A/Residues: 1-137 <HAR>

A/Cross-references: EMBL:X54435; NID:937812; PIDN:CAA8304.1; PID:937813

R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nollins,

Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23719

A/Molecule type: mRNA

A/Residues: 20-116 <HAW>

A/Cross-references: EMBL:X54435

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-137/Product: Ig heavy chain (fragment) #status predicted <MAT>

F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 461.5; DB 2; Length 137;

Best Local Similarity 76.5%; Pred. No. 1.5e-34;

Matches 91; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKGLWVAYISGGSGTYY 60

20 EVOLVSGGGGLVPGGSLRVSCAASGFTSSYMSWVROAPGKGLWVAINIKODGSEKTY 78

61 SDVSKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGGTLLTVSS 119

79 ADVSKRFTISRDNKNTLYLQNRSLRADDSAVYCARICGGTNSPDSWGGTLLTVSS 137

RESULT 36

S46390

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_rev: 27-Jan-1995 #text_change: 20-Jun-2000

C/Accession: S46390

R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31686; NID:9509782; PIDs:CAA83491.1; PID:g1335143
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 459.5; DB 2; Length 114;
Best Local Similarity 77.3%; Pred. No. 1.9e-34;
Matches 92; Conservative 6; Mismatches 16; Indels 5; Gaps 1;

Qy 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWNAVYISGSGSTYY 60
D 1 EVOLVESGGGVDPGRLRLSCAASGFTFSYAMHWVRQAPGKLEWNAVYISDGSNKYY 60

Qy 61 SDVKGRFTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYFPDSWQGTLLTV 119
D 61 ADSVKGRFTISRDNKNTLYLQWNSLEAEDTAVYYCAR-----DWGDYWGQGTLLTV 114

RESULT 37
Ig heavy chain precursor V-III region (38) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Oct-1996
C;Accession: A30532
R;Meeker, T.C.; Grimaldi, J.C.; O'Rourke, R.; Loeb, J.; Julinason, G.; Einhorn, S.
J. Immunol. 141, 3994-3998, 1988
A;Title: Lack of detectable somatic hypermutation in the V region of the Ig H chain gene
A;Reference number: A30532; MUID:89035542; PMID:3141510
A;Accession: A30532
A;Molecule type: DNA
A;Residues: 1-140 <ME>
A;Cross-references: GB:M23110
C;Genetics:
A;Intons: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;20-110/Product: Ig heavy chain V-III region 38 #status predicted <MAR>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 459; DB 2; Length 140;
Best Local Similarity 73.2%; Pred. No. 2.6e-34;
Matches 90; Conservative 12; Mismatches 15; Indels 6; Gaps 2;

Qy 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWNAVYISGSGSTYY 60
D 20 EVOLVESGGGVDPGSLRLSCAASGFTFSNYVMWVRQAPGKLEWVSSISGSDGTTY 79

Qy 61 SDVKGRFTISRDNKNTLYLQWRSLEAEDSAVYFCTR-----YKLGTYRDSWGQGTLLT 116
D 80 TAAVKGRTISRDNKNTLYLQWNSLEAEDTAVYYCAQNMGRDLRTPLAY--WGQGTLLTV 137

Qy 117 VSS 119
D 138 VSS 140

RESULT 38
S31669
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31669
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31685
A;Accession: S31669

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CUI>
A;Cross-references: EMBL:Z14212; NID:930959; PIDs:CAA78581.1; PID:g30960
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.5%; Score 458.5; DB 2; Length 141;
Best Local Similarity 73.8%; Pred. No. 2.9e-34;
Matches 90; Conservative 13; Mismatches 16; Indels 3; Gaps 1;

Qy 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWNAVYISGSGSTYY 60
D 20 EVOLVESGGGVDPGSLRLSCAASGFTFSYAMHWVRQAPGKLEWNAVYISSSSTYY 79

Qy 61 SDVKGRFTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYFPDSWQGTLLTV 117
D 80 ADSVKGRFTISRDNKNTLYLQWNSLEAEDTAVYYCARGRHLLTGKGYFDLWGRGTLTV 139

Qy 118 SS 119
D 140 SS 141

RESULT 39
E36005
Ig heavy chain V region (M72) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: E36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: E36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
A;Cross-references: GB:M34030
C;Genetics:
A;Gene: CDB:IGH@; IGHDI
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 457.5; DB 2; Length 122;
Best Local Similarity 74.6%; Pred. No. 3e-34;
Matches 91; Conservative 8; Mismatches 20; Indels 3; Gaps 1;

Qy 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWNAVYISGSGSTYY 60
D 1 QVOLVESGGGVDPGSLRLSCAASGFTFSYAMHWVRQAPGKLEWNAVYISDGSNKYY 60

Qy 61 SDVKGRFTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYFPDSWQGTLLTV 117
D 61 ADSVKGRFTISRDNKNTLYLQWNSLEAEDTAVYYCARDSHSSWYYGMDVWGQGTLLTV 120

Qy 118 SS 119
D 121 SS 122

RESULT 40
S26794
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: S26794
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene faml
A;Reference number: S26786; MUID:9211632; PMID:1730251
A;Accession: S26794
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <MOR>
A;Cross-references: EMBL:X61011
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 457; DB 2; Length 123;
Best Local Similarity 73.2%; Pred. No. 3.4e-34;
Matches 90; Conservative 11; Mismatches 18; Indels 4; Gaps 2;

QY	1	EVOLVESGDEFOVPGGSLRVSCAAGFASHYAMSWYRQAPGKGLWVAYISSGSGTYY	60
DB	1	EVOLVESGGGLVOPGSLRLSCAASGFTSSISIMNWYRQAPGKGLWVSTISSSTITY	60
QY	61	SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTR-VKL--GTYFPDSMGQTLLT	116
DB	61	ADSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTR-VKL--GTYFPDSMGQTLLT	120
QY	117	VSS	119
DB	121	VSS	123

Search completed: December 17, 2004, 18:30:18
Job time : 48.7978 secs

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GenCore version 5.1.6
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OM protein - pirotein search, using sw model

Run on: December 17, 2004, 18:29:23 ; Search time 355.663 Seconds
(without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-9

Perfect score: 624
Sequence: 1 EVQLVESGDFVPGGSLRV.....KLGTYYFDSWGCTLLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469	75.2	121	2 Q9UL71	Q9UL71 homo sapien
2	466	74.7	128	2 BAD00406	Bad00406 camelus d
3	460	73.7	128	2 BAD00444	Bad00444 camelus d
4	459.5	73.6	471	2 AAH24289	Aah24289 homo sapi
5	459	73.6	117	2 AAL35877	Aal35877 lama glam
6	457	73.2	124	2 BAD00534	Bad00534 camelus d
7	456	73.1	464	2 Q6MZ06	Q6mz06 homo sapien
8	456	73.1	464	2 CAE45931	CaE45931 homo sapi
9	456	73.1	470	2 Q6PXA4	Q6pja4 homo sapien
10	455	73.1	125	2 BAD00491	Bad00491 homo sapi
11	455.5	73.0	613	2 Q8WUK1	Q8wuk1 homo sapien
12	455.5	73.0	613	2 Q9UL90	Q9ul90 homo sapien
13	455	72.9	597	2 Q96BB9	Q96bb9 homo sapien
14	455	72.8	478	2 Q6P181	Q6p181 homo sapien
15	454	72.8	478	2 AAH41037	Aah41037 homo sapi
16	454	72.6	119	2 AAL35865	Aal35865 lama glam
17	453	72.6	118	2 Q9UL91	Q9ul91 homo sapien
18	451.5	72.4	124	2 BAD00233	Bad00233 camelus d
19	451.5	72.4	606	2 Q6GM72	Q6gm72 homo sapien
20	449.5	72.0	125	2 BAD00448	Bad00448 camelus d
21	449.5	72.0	126	2 BAD00510	Bad00510 camelus d
22	448.5	71.9	118	2 Q9UL72	Q9ul72 homo sapien
23	448.5	71.9	121	2 BAD00459	Bad00459 camelus d
24	448.5	71.9	475	2 Q6MZ06	Q6mz06 homo sapien
25	448.5	71.9	475	2 CAE45972	CaE45972 homo sapi
26	447	71.6	493	2 Q6GMX2	Q6gmx2 homo sapien
27	447	71.6	126	2 BAD00225	Bad00225 camelus d
28	446.5	71.5	119	2 Q920E7	Q920e7 mus musculu
29	446	71.5	126	2 BAD00420	Bad00420 camelus d
30	446	71.5	126	2 BAD00525	Bad00525 camelus d
31	445.5	71.4	121	2 BAD00525	Bad00525 camelus d

32	444	71.2	122	2 BAD00446	Bad00446 camelus d
33	444	71.2	122	2 BAD00549	Bad00549 camelus d
34	443.5	71.1	118	2 AAL35882	Aal35882 lama glam
35	443.5	71.1	129	2 BAD00424	Bad00424 camelus d
36	443.5	71.1	473	2 Q6MZV7	Q6mzv7 homo sapien
37	443.5	71.1	473	2 CAE45920	CaE45920 homo sapi
38	443	71.0	116	2 Q9UL93	Q9ul93 homo sapien
39	443	71.0	117	2 AAL35875	Aal35875 lama glam
40	442.5	70.9	125	2 BAD00490	Bad00490 camelus d
41	442.5	70.9	131	2 BAD00494	Bad00494 camelus d
42	442.5	70.9	465	2 Q6PEC4	Q6pec4 homo sapien
43	442.5	70.8	465	2 CAH62335	CaH62335 homo sapi
44	441.5	70.8	127	2 BAD00445	Bad00445 camelus d
45	441	70.7	124	2 BAD00513	Bad00513 camelus d

ALIGNMENTS

RESULT 1	ID	Q9UL71	PRELIMINARY;	PRT;	121 AA.
AC	Q9UL71				
DT	01-MAY-2000 (Tremblrel. 13, Created)				
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)				
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)				
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).				
DE	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9827139; PubMed=9614934;				
RA	Yu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL; AF035043; AAD56279.1; -.				
DR	HSSP; P01852; INF.				
DR	Interpro; IPR007110; Ig-like.				
DR	Interpro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PSS0835; IG_LIKE; 1.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE 121 AA; 13154 MW; 2F045CCFASD50736 CRC64;				
Query Match		75.2%;	Score 469;	DB 2;	Length 121;
Best Local Similarity		74.4%;	Pred. No. 2.4e-41;		
Matches	90;	Conservative 11;	Mismatches 18;	Indels 2;	Gaps 1;
Qy	1	EVQLVDSGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPEGKLEWVAISSGSGITY 60			
Db	1	EVQLVDSGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPEGKLEWVAISSGSGITY 60			
Qy	61	SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVFCTRYKLTYY--PDSWGCTLLTVS 118			
Db	61	ADSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVFCTRYKLTYY--PDSWGCTLLTVS 120			
Qy	119	S 119			
Db	121	S 121			
RESULT 2					
ID	BAD00406	PRELIMINARY;	PRT;	128 AA.	
AC	BAD00406;				
DT	02-MAR-2004 (Tremblrel. 27, Created)				

DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Immunoglobulin heavy chain VHDJ region (Fragment).
 GN IGVH.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Honda T.; Akahori Y.; Kurosawa Y.;
 RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
 RT gamma3 in vivo repertoire.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB092044; BAD00406.1; -.
 FT NON_TER 1
 FT NON_TER 128
 SQ SEQUENCE 128 AA; 13856 MW; 7C23CF09C28B889A CRC64;

Query Match 74.7%; Score 466; DB 2; Length 128;
 Best Local Similarity 69.6%; Pred. No. 5.4e-41;
 Matches 87; Conservative 16; Mismatches 16; Indels 6; Gaps 1;

QY 1 EVOLVESGGGVDPGGSLRVSCAASGPAFESHYAMSWVRQAPGKLEWVAIYSSGGSGTTY 60
 DB 1 EVOLVESGGGVDPGGSLRVSCAASGPAFESHYAMSWVRQAPGKLEWVAIYSSGGSGTTY 60
 QY 61 SDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTRVLT-----GTYFPGSWGQTL 114
 DB 61 ADSVKGRTISRDNKNTLYLQMSLRADSAVYFCTRVLT-----GTYFPGSWGQTL 120

QY 115 LTVSS 119
 DB 121 VTSS 125

RESULT 3
 BAD00444 PRELIMINARY; PRT; 128 AA.

AC BAD00444;
 DT 02-MAR-2004 (TReMBLrel. 27, Created)
 DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Immunoglobulin heavy chain VHDJ region (Fragment).
 GN IGVH.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Honda T.; Akahori Y.; Kurosawa Y.;
 RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
 RT gamma3 in vivo repertoire.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB092042; BAD00444.1; -.
 FT NON_TER 1
 FT NON_TER 128
 SQ SEQUENCE 128 AA; 13775 MW; 85B9EDD39D915993 CRC64;

Query Match 73.7%; Score 460; DB 2; Length 128;
 Best Local Similarity 71.0%; Pred. No. 2.3e-40;
 Matches 88; Conservative 13; Mismatches 17; Indels 6; Gaps 1;

QY 2 VOLVESGGGVDPGGSLRVSCAASGPAFESHYAMSWVRQAPGKLEWVAIYSSGGSGTTY 61
 DB 2 VOLVESGGGVDPGGSLRVSCAASGPAFESHYAMSWVRQAPGKLEWVAIYSSGGSGTTY 61
 QY 62 DSVMKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVK-----LGTTFPDSWGQTL 115
 DB 62 DSVMKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVK-----LGTTFPDSWGQTL 121

QY 116 TVSS 119
 DB 122 TISS 125

RESULT 4
 AAH24289 PRELIMINARY; PRT; 471 AA.

AC AAH24289;
 DT 02-MAR-2004 (TReMBLrel. 27, Created)
 DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
 RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
 RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
 RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
 RA Brownstein M.J.; Uddin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
 RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;
 RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.V.; Huiyk S.W.;
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
 RA Fahy J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;
 RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
 RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
 RA Krzywinski M.I.; Skalski U.; Smalins D.E.; Schnerch A.; Schein J.E.;
 RA Jones S.J.; Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC024289; AAH24289.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 73.6%; Score 459.5; DB 2; Length 471;
 Best Local Similarity 73.8%; Pred. No. 1.2e-39;
 Matches 90; Conservative 15; Mismatches 14; Indels 3; Gaps 2;

QY 1 EVOLVESGGGVDPGGSLRVSCAASGPAFESHYAMSWVRQAPGKLEWVAIYSSGGSGTTY 60
 DB 20 EVOLVESGGGVDPGGSLRVSCAASGPAFESHYAMSWVRQAPGKLEWVAIYSSGGSGTTY 79
 QY 61 SDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTRVK-----VKGTY-YPDSWGQTLTY 117
 DB 80 ADSVKGRTISRDNKNTLYLQMSLRADSAVYFCTRVK-----VKGTY-YPDSWGQTLTY 139

QY 118 SS 119
 DB 140 SS 141

RESULT 5
 AAL35877 PRELIMINARY; PRT; 117 AA.

AC AAL35877;
 DT 02-MAR-2004 (TReMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE Immunoglobulin heavy chain variable domain (Fragment).
OS Lama glama (Llama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2007448; PubMed=12009207;
RT Tanha J., Dubuc G., Hirama T., Narang S.A., Mackenzie C.R.;
RT "selection by phage display of llama conventional V(H) fragments with
RT heavy chain antibody V(H)H properties."
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL; AF442946; AAL35877.1; -.
FT NON TER 1 1
FT SEQUENCE 117 AA; 12459 MW; 08F5E4BA02F9801 CRC64;
SQ

Query Match 73.6%; Score 459; DB 2; Length 117;
Best Local Similarity 73.1%; Pred. No. 2.6e-40;
Matches 87; Conservative 14; Mismatches 16; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFHSYMSWRQAPGKLEWVAIYSSGSGTYY 60
DB 1 EVOLVSGGGLVPGGSLRVSCAASGTFPSYMSWRQAPGKLEWVSSINSGSGSTYY 60
QY 61 SDSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLTGYFPDWMGGTLLTVSS 119
DB 61 ADSVKGFTISRDNKNTLYLQMRSLKEPDALTYCARTRGSH--DYWGQGTIVTSS 117

RESULT 6

ID BAD00534 PRELIMINARY; PRT; 124 AA.
AC BAD00534;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SpLien;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092172; BAD00534.1; -.
FT NON TER 1 1
FT SEQUENCE 124 AA; 13421 MW; B31996777375A27E CRC64;
SQ

Query Match 73.2%; Score 457; DB 2; Length 124;
Best Local Similarity 70.2%; Pred. No. 4.6e-40;
Matches 85; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFHSYMSWRQAPGKLEWVAIYSSGSGTYY 60
DB 1 QVOLVESGGLVPGGSLRVSCAASGTFPSYMSWRQAPGKLEWVSTIKSAAGSTYY 60
QY 61 SDSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLTGYFPDS--WGQGTLLTVS 118
DB 61 ADSVKGFTISRDNKNTLYLQMRSLKTEDTAMTYCANLEFGSVSPRGVGGGTQVTVS 120
QY 119 S 119
DB 121 S 121

RESULT 7

ID O6MZU6 PRELIMINARY; PRT; 464 AA.
AC O6MZU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DE Hypothetical protein DKFP686C15213.
GN Name=DKFP686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-sect; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGL1; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66B8A0ABC CRC64;
QY

Query Match 73.1%; Score 456; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 2.7e-39;
Matches 90; Conservative 13; Mismatches 15; Indels 2; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFHSYMSWRQAPGKLEWVAIYSSGSGTYY 59
DB 20 EVOLVESGGLVPGGSLRVSCAASGTFPSYMSWRQAPGKLEWVSSINSGSGSTYY 79
QY 60 YSDSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLTGYFPDWMGGTLLTVSS 119
DB 80 YADVKGFTISRDNKNTLYLQMRSLKEPDALTYCARTRGSH--DYWGQGTIVTSS 138

RESULT 8

ID CAE45931 PRELIMINARY; PRT; 464 AA.
AC CAE45931;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE Hypothetical protein DKFP686C15213.
GN DKFP686C15213.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
KM Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66B8A0ABC CRC64;
QY

Query Match 73.1%; Score 456; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 2.7e-39;
Matches 90; Conservative 13; Mismatches 15; Indels 2; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFSGHYMSWVRQAPGKLEWVAYISSGSGSTY 59
DB 20 EVOLVESGGGLVPGGSLRLSCAASGFTFSYSNMWVRQAPGKLEWVSSFSFGSYEY 79
QY 60 YDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFPDSWGQGLTLTVSS 119
DB 80 YDSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYCAR-DLGMFGLDYWGQGLTLTVSS 138

RESULT 9
Q6PJ4 PRELIMINARY; PRT; 470 AA.

AC 06PJ4; TISSUE=Primary B-Cells;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pabey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywanski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL, BC018747; AA018747.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; Cl-sec; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; IG1; 3.
DR SMART: SM00406; IG; 1.
DR PROSITE: PSS0835; IG_LIKE; 4.
DR PROSITE: PSS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 73.1%; Score 456; DB 2; Length 470;
Best Local Similarity 74.4%; Pred. No. 2.7e-39;
Matches 90; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFSGHYMSWVRQAPGKLEWVAYISSGSGSTY 60
DB 20 EVOLVESGGGLVPGGSLRLSCAASGFTFSYSNMWVRQAPGKLEWVANI KDGSEKYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY--YFDSWGQGLTLTVS 118
DB 80 VDSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYCAR-DGSSSWYRDMFDPWGQGLTLTVS 139

QY 119 S 119
DB 140 S 140

RESULT 10
AA018747 PRELIMINARY; PRT; 470 AA.

AC AA018747; TISSUE=Primary B-Cells;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pabey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywanski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL, BC018747; AA018747.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 73.1%; Score 456; DB 2; Length 470;
Best Local Similarity 74.4%; Pred. No. 2.7e-39;
Matches 90; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

DB 140 S 140

RESULT 11

BAD00491 PRELIMINARY; PRT; 125 AA.

AC BAD00491; 02-MAR-2004 (TReMBLrel. 27, Created)

DT 02-MAR-2004 (TReMBLrel. 27, last sequence update)

DE 02-MAR-2004 (TReMBLrel. 27, last annotation update)

GN Immunoglobulin heavy chain VHDJ region (Fragment).

OS Camelus dromedarius (Dromedary) (Arabian camel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.

OX NCBI_TaxID=9838;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Honda T., Akahori Y., Kurosawa Y.;

RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and gamma3 in vivo repertoires."

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF092129; BAD00491.1; -.

FT NON_TER 1

FT NON_TER 125

SO SEQUENCE 125 AA; 13593 MW; F1637892B028E48C CRC64;

Query Match 73.0%; Score 455.5; DB 2; Length 125;
Best Local Similarity 70.5%; Pred. No. 6,7e-40;
Matches 86; Conservative 17; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVOLVESGGDFVPGGSLRVSCAASGPAFSPHYAMSVWROAPGKLEWVAIYSSGGSGTTY 60
DB 1 EVOLVESGGGVVPGGSLRLSCAASGFTFSYGMHWVROAPGKLEWVAIYSSGGSGTTY 60
QY 61 SDSVKGRFTISRDNSTLTLYLQWNSLRABDSAVYFCTRYVLTGYT--PDSMGQTLTLTV 117
DB 61 TESVKGRFTISRDNSTLTLYLQWNSLRABDSAVYFCTRYVLTGYT--PDSMGQTLTLTV 120
QY 118 SS 119
DB 121 SS 122

RESULT 12

Q8WUK1 PRELIMINARY; PRT; 613 AA.

AC Q8WUK1; 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)

DE 01-MAR-2004 (TReMBLrel. 26, last annotation update)

GN IGHM protein.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.L., Collins F.S., Wagner L., Shennan C.M., Bhat N.K.,
Altechul S.F., Zeeberg B., Buxlow K.H., Schaefer C.F., Hsieh L.,
Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hong L.,
Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
Brownstein M.J., Udell T.B., Tohiyuki S., Cantinici P., Prange C.,
Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Rohs S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
Vallion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC020240; AAH20240.1; -.

DR PIR; F36005; F36005.

DR PIR; G36005; G36005.

DR PIR; PH1642; PH1642.

DR PIR; PH1643; PH1643.

DR PIR; PH1645; PH1645.

DR PIR; PH1646; PH1646.

DR PIR; PL0098; PL0098.

DR PIR; PL0120; PL0120.

DR PIR; S15590; S15590.

DR PIR; S31116; S31116.

DR PIR; S31119; S31119.

DR PIR; S70442; S70442.

DR HSSP; P01861; IAD0.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 4.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PSS0835; IG_LIKE; 5.

DR PROSITE; PSS0290; IG_MHC; UNKNOWN; 3.

SO SEQUENCE 613 AA; 67295 MW; 60C7F5950671B315 CRC64;

Query Match 73.0%; Score 455.5; DB 2; Length 613;
Best Local Similarity 75.0%; Pred. No. 4,2e-39;
Matches 90; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVOLVESGGDFVPGGSLRVSCAASGPAFSPHYAMSVWROAPGKLEWVAIYSSGGSGTTY 60
DB 20 QVQLVSGGQVVPGRSLRLSCAASGFTFSYGMHWVROAPGKLEWVAIYSSGGSGTTY 79
QY 61 SDSVKGRFTISRDNSTLTLYLQWNSLRABDSAVYFCTRYVLTGYT--PDSMGQTLTLTV 119
DB 80 ADSVKGRFTISRDNSTLTLYLQWNSLRABDSAVYFCTRYVLTGYT--PDSMGQTLTLTV 139

RESULT 13

Q9UL90 PRELIMINARY; PRT; 113 AA.

AC Q9UL90; 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)

DE 01-MAR-2004 (TReMBLrel. 26, last annotation update)

GN Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=9827139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berny S.M.,
RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RT Clin. Immunol. Immunopathol. 87:184-192 (1998).

RL EMBL; AF035024; AAD56260.1; -.

```
DR PIR, S78486, S78486.
DR HSP, P01772, 2F84.
DR InterPro, IPR007110, Ig-1like.
DR InterPro, IPR003596, Ig_v.
DR Pfam, PF00047, Ig, 1.
DR SMART, SM00406, Ig, 1.
DR PROSITE, PS00835, Ig_Like, 1.
DR PROSITE, PS00835, Ig_Like, 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA, 12437 MW, ED57FDD19086D07F CRC64;

Query Match 72.9%; Score 455; DB 2; Length 113;
Best Local Similarity 74.8%; Pred. No. 6.7e-40;
Matches 89; Conservative 8; Mismatches 16; Indels 6; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGFAFGHYAMSWVRQAPGKLEWVAIYSSGSGSTY 60
DB 1 EVOLVSGGGLVPGGSLRVSCAAGFSSSYGMWVRQAPGKLEWVAIIRDGSKY 60
DY 61 SDSVKGRFTISRDNKNTLYLQWRSIAPDSAVYFCTRVGLGTYYPDSWGQGLT 119
DY 61 ADSVKGRFTISRDNKNTLYLQWNSIAPEDTAVYYCAK-----DLNYWGQGLT 113

RESULT 14
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toibiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC015760, AA015760.1, -.
DR PIR, S05271, S05271.
DR PIR, S24260, S24260.
DR HSP, P01861, IADQ.
DR InterPro, IPR007110, Ig-1like.
DR InterPro, IPR003597, Ig_c1.
DR InterPro, IPR003596, Ig_v.
DR InterPro, IPR003596, Ig_v.
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DR Pfam, PF07654, Cl-sect, 4.
DR Pfam, PF00047, Ig, 1.
DR SMART, SM00406, Ig, 1.
DR PROSITE, PS00835, Ig_Like, 5.
DR PROSITE, PS00290, IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA, 65039 MW, 4FCA3AD8ECC263D9 CRC64;

Query Match 72.9%; Score 455; DB 2; Length 597;
Best Local Similarity 72.0%; Pred. No. 4.6e-39;
Matches 90; Conservative 12; Mismatches 17; Indels 6; Gaps 2;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGFAFGHYAMSWVRQAPGKLEWVAIYSSGSGSTY 60
DB 20 EVOLVSGGGLVPGGSLRVSCAAGFSSSYGMWVRQAPGKLEWVAIYSSGSGSTY 79
DY 61 SDSVKGRFTISRDNKNTLYLQWRSIAPDSAVYFCTRVGLGTYYPDSWGQGLT 114
DY 80 ADSVKGRFTISRDNKNTLYLQWNSIAPEDTAVYYCAKPRGVSAGNTYRDEYWGQGLT 139

QY 115 LVVSS 119
DB 140 VTVSS 144

RESULT 15
Q6P181 PRELIMINARY; PRT; 478 AA.
AC Q6P181;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toibiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC041037, AA041037.1, -.
DR InterPro, IPR003599, Ig.
DR InterPro, IPR007110, Ig-1like.
DR InterPro, IPR003597, Ig_c1.
DR InterPro, IPR003596, Ig_v.
DR Pfam, PF07654, Cl-sect, 3.
DR Pfam, PF00047, Ig, 4.
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DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED3BD917970D6 CRC64;

Query Match 72.8%; Score 454; DB 2; Length 478;
Best Local Similarity 71.3%; Pred. No. 4,5e-39;
Matches 92; Conservative 7; Mismatches 20; Indels 10; Gaps 2;

QY 1 EVOLVESGDDFVQPGSLRVSCAASGFAFSHYAMSVWROAPGKLEWVAYISSGSGCTTY 60
DB 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYMWVWROAPGKLEWVAVNIKODGSEKYY 79
QY 61 SDVSKRFTISRNQNTLYLQWRSLRARDNAVYFCTR-----YKGTTF--DSWG 110
DB 80 VDSVKRFTISRNNKNSLYLQNNSLRAEDTAVYCARPEFESTMTTNNADYYFYNDVWG 139
QY 111 OGTLTVSS 119
DB 140 KGTTVVSS 148

RESULT 16
AAH41037 PRELIMINARY; PRT; 478 AA.

AC AAH41037
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED3BD917970D6 CRC64;

Query Match 72.8%; Score 454; DB 2; Length 478;
Best Local Similarity 71.3%; Pred. No. 4,5e-39;
Matches 92; Conservative 7; Mismatches 20; Indels 10; Gaps 2;

QY 1 EVOLVESGDDFVQPGSLRVSCAASGFAFSHYAMSVWROAPGKLEWVAYISSGSGCTTY 60
DB 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYMWVWROAPGKLEWVAVNIKODGSEKYY 79
QY 61 SDVSKRFTISRNQNTLYLQWRSLRARDNAVYFCTR-----YKGTTF--DSWG 110
DB 80 VDSVKRFTISRNNKNSLYLQNNSLRAEDTAVYCARPEFESTMTTNNADYYFYNDVWG 139
QY 111 OGTLTVSS 119
DB 140 KGTTVVSS 148

RESULT 17
AAL35865 PRELIMINARY; PRT; 119 AA.

AC AAL35865
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain variable domain (fragment).
OS Lama glama (llama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
NCBI_TaxID=9844;
RX SEQUENCE FROM N.A.
RC MEDLINE=22007448; PubMed=12009207;
RA Tanha J., Dubuc G., Hirama T., Naring S.A., Mackenzie C.R.;
RT "Selection by phage display of llama conventional V(H) fragments with
heavy chain antibody V(H) properties.";
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL; AF442934; AAL35865.1; -.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 12650 MW; E4CD04BF367A2D7 CRC64;

Query Match 72.6%; Score 453; DB 2; Length 119;
Best Local Similarity 73.1%; Pred. No. 1,2e-39;
Matches 87; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

QY 1 EVOLVESGDDFVQPGSLRVSCAASGFAFSHYAMSVWROAPGKLEWVAYISSGSGCTTY 60
DB 1 EVOLVAGGGLVQPGGSLRLSCAASGFTFSYMWVWROAPGKLEWVAVNIKODGSEKYY 60
QY 61 SDVSKRFTISRNQNTLYLQWRSLRARDNAVYFCTRVLYGTYVDPDSGCGTLTVSS 119
DB 61 ADSVKRFTISRNNKNSLYLQNNSLRAEDTAVYCARAHGTYGARGSGWGQGTIVVSS 119

RESULT 18

ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -.


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DR PIR; PH0875; PH0875.
DR PIR; S21205; S21205.
DR PIR; S30531; S30531.
DR HSP; P01783; IIGC.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 72.4%; Score 451.5; DB 2; Length 118;
Best Local Similarity 74.6%; Pred. No. 1.6e-39;
Matches 88; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQAPGKGLWVAIYSSGGSGTTY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAAGFTFSYAMSVWRQAPGKGLWVAIYSSGGSGTTY 60
QY SDSVKRFTISRDNSKNTLYLQKRSIARAEDSAVYFCR-----VKGTTFPDSMGQTLTVS 118
DB 61 SDSVKRFTISRDNSKNTLYLQKRSIARAEDSAVYFCR-----VKGTTFPDSMGQTLTVS 115
DB 61 ADSVKRFTISRDNAKNTLYLQNSISLRAEDTAIVYCARGD-SEAPDIMGQGMVTVS 117
DB 61 ADSVKRFTISRDNAKNTLYLQNSISLRAEDTAIVYCARGD-SEAPDIMGQGMVTVS 117

RESULT 19
BAD00233 PRELIMINARY; PRT; 124 AA.
AC BAD00233;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoire."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091871; BAD00233.1; -.
FT NON TER 1
FT NON TER 124
SQ SEQUENCE 124 AA; 13374 MW; FE75B41506CABD25 CRC64;

Query Match 72.4%; Score 451.5; DB 2; Length 124;
Best Local Similarity 68.5%; Pred. No. 1.7e-39;
Matches 85; Conservative 15; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQAPGKGLWVAIYSSGGSGTTY 60
DB 1 OVOLOSSEGGGLVPGGSLRLSCAAGFTFSYAMSVWRQAPGKGLWVAIYSSGGSGTTY 60
QY SDSVKRFTISRDNSKNTLYLQKRSIARAEDSAVYFCR-----VKGTTFPDSMGQTLTVS 115
DB 61 ADSVKRFTISRDNAKNTLYLQNSISLRAEDTAIVYCARGD-SEAPDIMGQGMVTVS 117
DB 61 ADSVKRFTISRDNAKNTLYLQNSISLRAEDTAIVYCARGD-SEAPDIMGQGMVTVS 117

QY 116 TVSS 119
DB 121 TVSS 124

RESULT 20
Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
RA Diatchenko L., Marcusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Teichlyuk S., Carninci P., Prange S.C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellon E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-setc 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00250; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Query Match 72.4%; Score 451.5; DB 2; Length 606;
Best Local Similarity 67.2%; Pred. No. 1.1e-38;
Matches 90; Conservative 12; Mismatches 17; Indels 15; Gaps 2;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGFAFSHYAMSVWRQAPGKGLWVAIYSSGGSGTTY 60
DB 20 QVOVLESGGGLVPGGSLRLSCAAGFTFSYAMSVWRQAPGKGLWVAIYSSGGSGTTY 79
QY SDSVKRFTISRDNSKNTLYLQKRSIARAEDSAVYFCR-----VKGTTFPDSMGQTLTVS 106
DB 80 ADSVKRFTISRDNAKNTLYLQNSISLRAEDTAIVYCARGD-SEAPDIMGQGMVTVS 139
DB 80 ADSVKRFTISRDNAKNTLYLQNSISLRAEDTAIVYCARGD-SEAPDIMGQGMVTVS 139

QY 107 -DSMGQTLTVSS 119
DB 140 MDVWGQGITVTVSS 153

RESULT 21
BAD00448 PRELIMINARY; PRT; 125 AA.
AC BAD00448;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
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DR EMBL; AB092097; BAD00459.1; -.
 FT NON TER 1
 SQ SEQUENCE 121 AA; 12957 MW; A55F627A3F977A6D CRC64;

Query Match 71.9%; Score 448.5; DB 2; Length 121;
 Best Local Similarity 71.4%; Pred. No. 3,5e-39;
 Matches 85; Conservative 18; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGPFAFSHYAMSWROAPGKGLWVAYISSGSGCTTY 60
 DB 1 EVOLVSGGGLVPGGSLRLSCAASGFTFRNVMNWRQAPGKGLWVSHINSGGSNSWY 60

QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRYVLGTYYPDSWGQGLTVSS 119
 DB 61 ADSVKGRFTISRDNAKNTLYLQNSLKTEDTAVYYCVK-NPSTWYFELWGQGLTVSS 118

RESULT 25
 Q6M2Q6 PRELIMINARY; PRT; 475 AA.

AC Q6M2Q6; 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686G11190;
 GN Name=DKFZp686G11190;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RA SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG THE GERMAN HUMAN CDNA CONSORTIUM;
 RA Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Oanger A., Fobo G.,
 Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640947; CAE45972.1; -.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-1ike.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003066; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF07654; Cl-set; 3.
 DR Pfam: PF00047; IG; 4.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG1; 3.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.

QY SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 71.9%; Score 448.5; DB 2; Length 475;
 Best Local Similarity 69.0%; Pred. No. 1,7e-38;
 Matches 87; Conservative 13; Mismatches 19; Indels 7; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGPFAFSHYAMSWROAPGKGLWVAYISSGSGCTTY 60
 DB 20 EVOLVSGGGLVPGGSLRLSCAASGFTFRNVMNWRQAPGKGLWVSHINSGGSNTTY 79

QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRYVLGTY-----YFDSWGQGT 113
 DB 80 ADSVKGRFTISRDNSKNTLYLQMRSLRAEDTAVYYCARADYRDYQVSPAYWYFDVWGRT 139

QY 114 LRTVSS 119
 DB 140 LVSUSA 145

RESULT 26
 CAE45972

ID CAE45972 PRELIMINARY; PRT; 475 AA.

AC CAE45972;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686G11190;
 GN DKFZp686G11190.
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RA SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RA Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Oanger A., Fobo G.,
 Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640947; CAE45972.1; -.
 KW Hypothetical protein.
 QY SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 71.9%; Score 448.5; DB 2; Length 475;
 Best Local Similarity 69.0%; Pred. No. 1,7e-38;
 Matches 87; Conservative 13; Mismatches 19; Indels 7; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGPFAFSHYAMSWROAPGKGLWVAYISSGSGCTTY 60
 DB 20 EVOLVSGGGLVPGGSLRLSCAASGFTFRNVMNWRQAPGKGLWVSHINSGGSNTTY 79

QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRYVLGTY-----YFDSWGQGT 113
 DB 80 ADSVKGRFTISRDNSKNTLYLQMRSLRAEDTAVYYCARADYRDYQVSPAYWYFDVWGRT 139

QY 114 LRTVSS 119
 DB 140 LVSUSA 145

RESULT 27
 Q6GMX2 PRELIMINARY; PRT; 493 AA.

AC Q6GMX2; 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RA SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan D.M., Moore T., Max S.I., Wang J., Heist F.,
 Diatchenko L., Mansina K., Farmer A.R., Rubin G.M., Hong L.,
 Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hultky S.W.,
 Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.B.,
 Jones S.J., Marra M.A.;
 RT Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences. ";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RC SEQUENCE FROM N.A.
RA TISSUE=Spleen;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL: BC073771; AAH73771.1; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG C1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-set; 2.
DR Pfam: PF00047; IG; 3.
DR SMART: SM00409; IG; 4.
DR SMART: SM00407; IG1; 2.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_Like; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 52865 MW; 558999305B286203 CRC64;

Query Match 71.6%; Score 447; DB 2; Length 493;
Best Local Similarity 73.6%; Pred. No. 2.6e-38;
Matches 89; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFSHYMSVWRQAPGKLEWVAYISSGSGTYY 60
DB 20 EVOLVSGGGLVPGGSLRVSCAASGTFSSYMSVWRQAPGKLVWVSNINDGSTSY 79
QY 61 SDSVKGRFTISRDNKNLTLYLQMSLRAPDSAVYFCTR--VKLTGYYPDSMGGTLTVS 118
DB 80 ADSVKGRFTISRDNKNLTLYLQMSLRGEDAAVYCARGVSLPRSTLDIWGQTVMTVS 139
QY 119 S 119
DB 140 S 140

RESULT 28

BAD00225 PRELIMINARY; PRT; 126 AA.
ID BAD00225;
AC BAD00225;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AB091863; BAD00225.1; -
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 13717 MW; 486E1D741474EF26 CRC64;

Query Match 71.6%; Score 446.5; DB 2; Length 126;
Best Local Similarity 68.3%; Pred. No. 5.9e-39;
Matches 86; Conservative 17; Mismatches 16; Indels 7; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFSHYMSVWRQAPGKLEWVAYISSGSGTYY 60
DB 1 QVQLVDSGGGLVPGGSLRVSCAASGTFSSYMSVWRQAPGKLVWVSNINDGSTSY 60
QY 61 SDSVKGRFTISRDNKNLTLYLQMSLRAPDSAVYFCTRVL--GTYT-----PDSMGQGT 113

DB 61 ADSVKGRFTISRDNKNLTLYLQMSLRGEDAAVYCARGVSLPRSTLDIWGQTVMTVS 120
QY 114 LRTVSS 119
DB 121 QVTVSS 126

RESULT 29

Q920E7 PRELIMINARY; PRT; 119 AA.
ID Q920E7;
AC Q920E7;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Peptide-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaltis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF307937; AAL09421.1; -
DR PIR: C25913; C25913.
DR HSP: P01783; IIGC.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_Like; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6B90404381CA7C CRC64;

Query Match 71.5%; Score 446; DB 2; Length 119;
Best Local Similarity 73.6%; Pred. No. 6.3e-39;
Matches 89; Conservative 11; Mismatches 17; Indels 4; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFSHYMSVWRQAPGKLEWVAYISSGSGTYY 60
DB 1 EVOLVSGGGLVPGGSLRVSCAASGTFSSYMSVWRQAPGKLVWVSNINDGSTSY 60
QY 61 SDSVKGRFTISRDNKNLTLYLQMSLRAPDSAVYFCTRVLGTY--YFDSMGGTLTVS 118
DB 61 PDSVKGRFTISRDNKNLTLYLQMSLRGEDAAVYCAR--HGDDYDVFAWGGTLTVS 118
QY 119 S 119
DB 119 A 119

RESULT 30

BAD00420 PRELIMINARY; PRT; 126 AA.
ID BAD00420;
AC BAD00420;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFSHYMSVWRQAPGKLEWVAYISSGSGTYY 60
DB 1 QVQLVDSGGGLVPGGSLRVSCAASGTFSSYMSVWRQAPGKLVWVSNINDGSTSY 60
QY 61 SDSVKGRFTISRDNKNLTLYLQMSLRAPDSAVYFCTRVL--GTYT-----PDSMGQGT 113

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092058; BAD00420.1; -.
FT NON_TER 1 1
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13569 MW; A8F3B29E6C9BE29D CRC64;

Query Match
Best Local Similarity 71.5%; Score 446; DB 2; Length 126;
Matches 86; Conservative 15; Mismatches 16; Indels 8; Gaps 2;

QY 1 EVOLVSGGDFVOPGSLRVSCAASGPAFSPHYAMSWVROAPGKGLEWVAYISGSGSTYY 60
DB 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTSTYMSVWRQAPGKGLEWVAISNGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYIQWRSIPRAEDSAVYFCTRVKLGTYFPDS-----WGQGTLL 114
DB 61 ADSVKGRFTISRDNKNTLYIQWRSIPRAEDSAVYFCTRVKLGTYFPDS-----WGQGTLL 114
QY 115 LTVSS 119
DB 119 VTVSS 123

RESULT 31
BAD00525 PRELIMINARY; PRT; 121 AA.
AC BAD00525;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]_TaxID=9838;
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092163; BAD00525.1; -.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 12951 MW; A6D50E79D505E5B4 CRC64;

Query Match
Best Local Similarity 71.4%; Score 445.5; DB 2; Length 121;
Matches 85; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVOLVSGGDFVOPGSLRVSCAASGPAFSPHYAMSWVROAPGKGLEWVAYISGSGSTYY 60
DB 1 DVQLVSGGGLVOPGSGSLRLSCAASGFTSTYMSVWRQAPGKGLEWVAISNGSGSTYY 59
QY 61 SDSVKGRFTISRDNKNTLYIQWRSIPRAEDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 119
DB 60 ADSVKGRFTISRDNKNTLYIQWRSIPRAEDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 118

RESULT 32
BAD00446 PRELIMINARY; PRT; 122 AA.
AC BAD00446;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.

OX NCBI_TaxID=9838;
RN [1]_TaxID=9838;
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092084; BAD00446.1; -.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13395 MW; 27043A8FC3A4771D CRC64;

Query Match
Best Local Similarity 71.2%; Score 444; DB 2; Length 122;
Matches 84; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 EVOLVSGGDFVOPGSLRVSCAASGPAFSPHYAMSWVROAPGKGLEWVAYISGSGSTYY 60
DB 1 DVQLVSGGGLVOPGSGSLRLSCAASGFTSTYMSVWRQAPGKGLEWVAISNGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYIQWRSIPRAEDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYIQWRSIPRAEDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 119

RESULT 33
BAD00549 PRELIMINARY; PRT; 122 AA.
AC BAD00549;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]_TaxID=9838;
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092187; BAD00549.1; -.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13354 MW; 1DC6AF409EB3A526 CRC64;

Query Match
Best Local Similarity 71.2%; Score 444; DB 2; Length 122;
Matches 83; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 EVOLVSGGDFVOPGSLRVSCAASGPAFSPHYAMSWVROAPGKGLEWVAYISGSGSTYY 60
DB 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTSTYMSVWRQAPGKGLEWVAISNGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYIQWRSIPRAEDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 119
DB 61 PDSVKGRFTISRDNKNTLYIQWRSIPRAEDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 119

RESULT 34
AAL35882 PRELIMINARY; PRT; 118 AA.
AC AAL35882;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain variable domain (Fragment).
GN Lama glama (Llama).
OS

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22007448; PubMed=12009207;
RA Tanha J., Dubuc G., Hirama T., Narang S.A., Mackenzie C.R.;
RT "Selection by phase display of llama conventional V(H) fragments with
RT heavy chain antibody V(H)H properties.";
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL: AF442951; AAL35882.1; -.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12916 MW; B1127A094C166B57 CRC64;

Query Match 71.1%; Score 443.5; DB 2; Length 118;
Best Local Similarity 73.1%; Pred. No. 1.1e-38;
Matches 87; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

QY 1 EVOLVESGDPFVPGGSLRVSCAAGFAPSHYAMSWVROAPGKGLEWVAYISSGSGCTTY 60
DB 1 DVQLQASGGGLVPGGSLRVSCAAGFTFSNHYHVMVROAPGKGLEWVSTINIDGCTTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY--YFDSMGCGTLL 119
DB 61 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTALYYCVRDGCGTTRY-DYWGCGTQVTVSS 118

RESULT 35
BAD00424 PRELIMINARY; PRT; 129 AA.
ID BAD00424;
AC BAD00424;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGHV.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB092062; BAD00424.1; -.
FT NON_TER 1
FT NON_TER 129
SQ SEQUENCE 129 AA; 13971 MW; 243F7C8B1A436C50 CRC64;

Query Match 71.1%; Score 443.5; DB 2; Length 129;
Best Local Similarity 68.5%; Pred. No. 1.3e-38;
Matches 87; Conservative 12; Mismatches 19; Indels 9; Gaps 2;

QY 1 EVOLVESGDPFVPGGSLRVSCAAGFAPSHYAMSWVROAPGKGLEWVAYISSGSGCTTY 60
DB 1 DVQLVESGGGLVPGGSLRVSCAAGFTFSYNAMSWVROAPGKGLEWVSSISRAGATYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFDSMGCG 112
DB 61 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTGYCTQ-DPGDYSDATWTSQNGYWGCG 119

QY 113 TLLTVSS 119
DB 120 TVTVSS 126

RESULT 36
Q6MZV7 PRELIMINARY; PRT; 473 AA.
ID Q6MZV7

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AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX40853; CAE45920.1; -.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 52121 MW; 9476BAE4C0BFC447 CRC64;

Query Match 71.1%; Score 443.5; DB 2; Length 473;
Best Local Similarity 66.9%; Pred. No. 5.7e-38;
Matches 83; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

QY 1 EVOLVESGDPFVPGGSLRVSCAAGFAPSHYAMSWVROAPGKGLEWVAYISSGSGCTTY 60
DB 20 EIVLVSGGGLVPGGSLRVSCAAGFTFSFEMNVVROAPGKGLEWVAYITSGNTVY 79

QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY----YFDSMGCGTLL 115
DB 80 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYCARQNEHTSPWYPSFDYWGCGILV 139

QY 116 TVSS 119
DB 140 TVSS 143

RESULT 37
CAE45920 PRELIMINARY; PRT; 473 AA.
ID CAE45920;
AC CAE45920;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN DKFZp686C11235.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX40853; CAE45920.1; -.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 52121 MW; 9476BAE4C0BFC447 CRC64;

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Query Match      71.1%; Score 443.5; DB 2; Length 473;
Best Local Similarity 66.9%; Pred. No. 5,7e-36;
Matches 83; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSPHYMSWVRQAPGKLEWVAIYSSGGSGTTY 60
DB 20 EIQVLESGGGLVQPGGSLRVSCAASGFTFSSPYHMAVRQAPGKLEWVAIYSSGGTY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYPDSSWGGTLL 115
DB 80 ADSLQGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARQMRHNSPMYPSFDFWGGIIV 139
QY 116 TVSS 119
DB 140 TVSS 143

RESULT 38
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Myosin-reactive Immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR PIR; PH1644; PH1644.
DR PIR; P10120; P10120.
DR HSP; P01772; 2F84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match      71.0%; Score 443; DB 2; Length 116;
Best Local Similarity 76.5%; Pred. No. 1,3e-38;
Matches 91; Conservative 6; Mismatches 18; Indels 4; Gaps 2;

QY 2 VOLVESGDFVPGGSLRVSCAASGFAFSPHYMSWVRQAPGKLEWVAIYSSGGSGTTY 61
DB 1 VOLVESGGGLVQPGGSLRVSCAASGFTFSSPYHMAVRQAPGKLEWVAIYSSGGTY 60
QY 62 DSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYPDSSWGGTLL 119
DB 61 DSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARQMRHNSPMYPSFDFWGGIIV 116

RESULT 39
AAL35875 PRELIMINARY; PRT; 117 AA.
AC AAL35875;
DT 02-MAR-2004 (TREMblrel. 27, Created)
DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
DE Immunoglobulin heavy chain variable domain (Fragment).
DE Lama glama (Llama).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22007448; PubMed=12009207;
RA Tanha J., Dubuc G., Hirama T., Narang S.A., Mackenzie C.R.;
RT "Selection by phage display of llama conventional VH fragments with
RT heavy chain antibody V(H)H properties.";
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL; AF442944; AAL35875.1; -.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 12416 MW; CA010A137CB01461 CRC64;

Query Match      71.0%; Score 443; DB 2; Length 117;
Best Local Similarity 71.4%; Pred. No. 1,3e-38;
Matches 85; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSPHYMSWVRQAPGKLEWVAIYSSGGSGTTY 60
DB 1 EVOLASGGGLVQPGGSLRVSCAASGFTFSSPYHMAVRQAPGKLEWVAIYSSGGTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYPDSSWGGTLL 119
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARQMRHNSPMYPSFDFWGGIIV 117

RESULT 40
BAD00490 PRELIMINARY; PRT; 125 AA.
AC BAD00490;
DT 02-MAR-2004 (TREMblrel. 27, Created)
DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHD region (Fragment).
DE IGVH.
GN Camelus dromedarius (Dromedary) (Arabian camel).
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092128; BAD00490.1; -.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13518 MW; F11D6CBE62BD171 CRC64;

Query Match      70.9%; Score 442.5; DB 2; Length 125;
Best Local Similarity 70.5%; Pred. No. 1,5e-38;
Matches 86; Conservative 12; Mismatches 21; Indels 3; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSPHYMSWVRQAPGKLEWVAIYSSGGSG 57
DB 1 QVOLVESGGGLVQPGGSLRVSCAASGFTFSSPYHMAVRQAPGKLEWVAIYSSGGTY 60
QY 58 TVYSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYPDSSWGGTLL 117
DB 61 TVYSDSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARQMRHNSPMYPSFDFWGGIIV 120

QY 118 SS 119
DB 121 SS 122

Search completed: December 17, 2004, 19:14:45
Job time : 356.663 secs

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